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OM protein - protein search, using sw model

Run on: April 16, 2005, 03:28:04 ; Search time 136 Seconds
(without alignments)
674.517 Million cell updates/sec

Title: US-10-753-079-1

Perfect score: 1528

Sequence: 1 DSEDESHITITDELPLK.....RRKKQRVKIAYEISIFVKQM 276

Scoring table:

Blosum62

Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370683 residues

Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
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20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1528	100.0	276	9	US-09-766-778-1
2	1528	100.0	276	13	US-10-086-176A-5
3	1528	100.0	276	14	US-10-270-478-1
4	1528	100.0	276	14	US-10-270-479-1
5	1528	100.0	276	16	US-10-753-079-1
6	1528	100.0	276	17	US-10-753-078A-1
7	1528	100.0	277	14	US-10-270-478-2
8	1528	100.0	277	14	US-10-270-479-2
9	1528	100.0	304	14	US-10-167-351-1
10	1528	100.0	304	16	US-10-755-889-412
11	1528	100.0	352	17	US-10-860-277-2
12	1525	99.8	276	9	US-09-741-106-9
13	1525	99.8	276	17	US-10-918-366-9

14	1525	99.8	276	17	US-10-860-277-3	Sequence 3, Appli
15	1522	99.6	304	14	US-10-377-817-2	Sequence 2, Appli
16	1447.5	94.7	291	10	US-09-992-600A-48	Sequence 48, Appli
17	1447.5	94.7	291	10	US-09-924-340-48	Sequence 48, Appli
18	1447.5	94.7	291	10	US-09-992-095B-48	Sequence 48, Appli
19	1447.5	94.7	291	10	US-09-999-570-48	Sequence 48, Appli
20	1447.5	94.7	291	14	US-10-000-489-48	Sequence 48, Appli
21	1447.5	94.7	291	14	US-10-000-986-48	Sequence 48, Appli
22	1447.5	94.7	291	14	US-10-154-678-48	Sequence 48, Appli
23	1447.5	94.7	291	17	US-10-838-854-48	Sequence 48, Appli
24	1444.5	94.5	291	10	US-09-992-600A-52	Sequence 52, Appli
25	1444.5	94.5	291	10	US-09-924-340-52	Sequence 52, Appli
26	1444.5	94.5	291	10	US-09-992-095B-52	Sequence 52, Appli
27	1444.5	94.5	291	10	US-09-999-570-52	Sequence 52, Appli
28	1444.5	94.5	291	14	US-10-000-489-52	Sequence 52, Appli
29	1444.5	94.5	291	14	US-10-000-986-52	Sequence 52, Appli
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31	1444.5	94.5	291	17	US-10-838-854-52	Sequence 52, Appli
32	901	59.0	160	15	US-10-408-166-472	Sequence 472, App
33	897	58.7	161	9	US-09-741-106-19	Sequence 19, Appli
34	897	58.7	161	17	US-10-918-366-19	Sequence 19, Appli
35	745	48.8	164	10	US-09-992-600A-96	Sequence 96, Appli
36	745	48.8	164	10	US-09-924-340-96	Sequence 96, Appli
37	745	48.8	164	10	US-09-992-095B-96	Sequence 96, Appli
38	745	48.8	164	10	US-09-999-570-96	Sequence 96, Appli
39	745	48.8	164	14	US-10-000-489-96	Sequence 96, Appli
40	745	48.8	164	14	US-10-000-986-96	Sequence 96, Appli
41	745	48.8	164	14	US-10-154-678-96	Sequence 96, Appli
42	745	48.8	164	17	US-10-838-854-96	Sequence 96, Appli
43	660	43.2	152	10	US-09-992-600A-94	Sequence 94, Appli
44	660	43.2	152	10	US-09-924-340-94	Sequence 94, Appli
45	660	43.2	152	10	US-09-992-095B-94	Sequence 94, Appli

ALIGNMENTS

RESULT 1
US-09-766-778-1
; Sequence 1, Application US/09766778
; Patent No. US20010018204A1
; GENERAL INFORMATION:
; APPLICANT: Papathanassiou, Adonia E
; Green, Shawn J.
; TITLE OF INVENTION: Compositions and Methods for Inhibiting Cellular Proliferation
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew
; STREET: 191 Peachtree Street, 37th Floor
; City: Atlanta
; STATE: Georgia
; COUNTRY: U.S.A.
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/766,778
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/227,955
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Greene, Jamie L.
; REGISTRATION NUMBER: 32,467
; REFERENCE/DOCKET NUMBER: 05213-0290
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 818-3700
; TELEFAX: (404) 818-3799

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: Active-site
LOCATION: 2..3
OTHER INFORMATION: /note= "Site of partial phosphorylation"
FEATURE:
NAME/KEY: Active-site
LOCATION: 117..118
OTHER INFORMATION: /note= "Potential site for N-linked glycosylation"
FEATURE:
NAME/KEY: Active-site
LOCATION: 167..168
OTHER INFORMATION: /note= "Potential site for N-linked glycosylation"
FEATURE:
NAME/KEY: Active-site
LOCATION: 228..229
OTHER INFORMATION: /note= "Potential site for N-linked glycosylation"
FEATURE:
NAME/KEY: Domain
LOCATION: 26..76
OTHER INFORMATION: /label= Kunitz-1
FEATURE:
NAME/KEY: Domain
LOCATION: 97..147
OTHER INFORMATION: /label= Kunitz-2
FEATURE:
NAME/KEY: Domain
LOCATION: 189..239
OTHER INFORMATION: /label= Kunitz-3
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-766-778-1
Query Match 100.0%; Score 1528; DB 9; Length 276;
Best Local Similarity 100.0%; Pred. No. 6.6e-137; Mismatches 0; Indels 0; Gaps 0;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DSEDEHTIITDELPLKLMHSFCFAKADGPKAKMKEFFNIFTRQCEEFYGGCE 60
Db 1 DSEDEHTIITDELPLKLMHSFCFAKADGPKAKMKEFFNIFTRQCEEFYGGCE 60
Qy 61 GNQRFESLECKKMCCTRDNANRIIKTTLOEKDFCFLEEDPGICRGYITRYFNNQTK 120
Db 61 GNQRFESLECKKMCCTRDNANRIIKTTLOEKDFCFLEEDPGICRGYITRYFNNQTK 120
Qy 121 QCFERFKYGGCLGNMNNFETLECKNICEDGPNQGVNDNYGTQLNAVNNSLTPQSTKVP 180
Db 121 QCFERFKYGGCLGNMNNFETLECKNICEDGPNQGVNDNYGTQLNAVNNSLTPQSTKVP 180
Qy 181 FEFHGPSWCLTPADRGICRANENRFFYNSVIGKCRPFKYSKCGGNNNNFTSKQEC 240
Db 181 FEFHGPSWCLTPADRGICRANENRFFYNSVIGKCRPFKYSKCGGNNNNFTSKQEC 240
Qy 241 KGFQIRISKGLIKTKRKKQKVIAEYEIFVKNM 276
Db 241 KGFQIRISKGLIKTKRKKQKVIAEYEIFVKNM 276
RESULT 2

US-10-086-176A-5
Sequence 5, Application US/10086176A
Publication No. US20020173465A1
GENERAL INFORMATION:
APPLICANT: Hembrough, Todd
APPLICANT: Papathanasiou, Adonia E.
APPLICANT: Green, Shawn J.
TITLE OF INVENTION: Compositions and Methods for Inhibiting Cellular Proliferation Co
FILE REFERENCE: 05213-0296 43170-266780
CURRENT APPLICATION NUMBER: US/10/086.176A
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 09/766,778
PRIOR FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: US 09/227,955
PRIOR FILING DATE: 1999-01-11
PRIOR APPLICATION NUMBER: US 08/796,850
PRIOR FILING DATE: 1997-02-06
PRIOR APPLICATION NUMBER: US 09/130,273
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent in version 3.1
SEQ ID NO 5
LENGTH: 276
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-10-086-176A-5
Query Match 100.0%; Score 1528; DB 13; Length 276;
Best Local Similarity 100.0%; Pred. No. 6.6e-137; Mismatches 0; Indels 0; Gaps 0;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DSEDEHTIITDELPLKLMHSFCFAKADGPKAKMKEFFNIFTRQCEEFYGGCE 60
Db 1 DSEDEHTIITDELPLKLMHSFCFAKADGPKAKMKEFFNIFTRQCEEFYGGCE 60
Qy 61 GNQRFESLECKKMCCTRDNANRIIKTTLOEKDFCFLEEDPGICRGYITRYFNNQTK 120
Db 61 GNQRFESLECKKMCCTRDNANRIIKTTLOEKDFCFLEEDPGICRGYITRYFNNQTK 120
Qy 121 QCFERFKYGGCLGNMNNFETLECKNICEDGPNQGVNDNYGTQLNAVNNSLTPQSTKVP 180
Db 121 QCFERFKYGGCLGNMNNFETLECKNICEDGPNQGVNDNYGTQLNAVNNSLTPQSTKVP 180
Qy 181 FEFHGPSWCLTPADRGICRANENRFFYNSVIGKCRPFKYSKCGGNNNNFTSKQEC 240
Db 181 FEFHGPSWCLTPADRGICRANENRFFYNSVIGKCRPFKYSKCGGNNNNFTSKQEC 240
Qy 241 KGFQIRISKGLIKTKRKKQKVIAEYEIFVKNM 276
Db 241 KGFQIRISKGLIKTKRKKQKVIAEYEIFVKNM 276
RESULT 3
US-10-270-478-1
Sequence 1, Application US/10270478
Publication No. US20030139339A1
GENERAL INFORMATION:
APPLICANT: Creasey, Abba
TITLE OF INVENTION: Treatment of Severe Pneumonia by
FILE REFERENCE: 012441.00027
CURRENT APPLICATION NUMBER: US/10/270,478
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US 60/328,806
PRIOR FILING DATE: 2001-10-15
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 276
TYPE: PRT

;; PRIOR APPLICATION NUMBER: US 60/509,277
;; PRIOR FILING DATE: 2003-10-08
;; PRIOR APPLICATION NUMBER: US 60/512,199
;; PRIOR FILING DATE: 2003-10-20
;; NUMBER OF SEQ ID NOS: 44
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1
;; LENGTH: 276
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-753-078A-1

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Best Local Similarity 100.0%; Pred. No. 6.6e-137;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 DSEDEBHTIITDTELPPLKMHSCAFKADGPKAIMKRFNFITRQCEEFYGGCE 60

QY 61 GNONRFESLECKKCTRDNANRIIKTTLQOEKPDFCFLEEDPGICRGYITRYFYNNOTK 120
DB 61 GNONRFESLECKKCTRDNANRIIKTTLQOEKPDFCFLEEDPGICRGYITRYFYNNOTK 120

QY 121 QCFERFYGGCLGNMNFETLECKNICEDGPNQFQVDNYGTQLNANNSLTPQSTKVP 180
DB 121 QCFERFYGGCLGNMNFETLECKNICEDGPNQFQVDNYGTQLNANNSLTPQSTKVP 180

QY 181 FEHGPSWCLTPADRGGLCRANENRYNSVIGKCRPFKYSGCCGNNFTSKQECRLACK 240
DB 181 FEHGPSWCLTPADRGGLCRANENRYNSVIGKCRPFKYSGCCGNNFTSKQECRLACK 240

QY 241 KGFQIRISKGGLIKTKRKRKQKRVKIAVEEIFVKNM 276
DB 241 KGFQIRISKGGLIKTKRKRKQKRVKIAVEEIFVKNM 276

RESULT 7
US-10-270-478-2
;; Sequence 2, Application US/10270478
;; Publication No. US2003013939A1
;; GENERAL INFORMATION:
;; APPLICANT: Creasey, Abba
;; TITLE OF INVENTION: Treatment of Severe Pneumonia by
;; TITLE OF INVENTION: Administration of Tissue Factor Pathway Inhibitor (TFPI)
;; FILE REFERENCE: 012441.00027
;; CURRENT APPLICATION NUMBER: US/10/270,478
;; PRIOR FILING DATE: 2002-10-15
;; PRIOR APPLICATION NUMBER: US 60/328,806
;; PRIOR FILING DATE: 2001-10-15
;; NUMBER OF SEQ ID NOS: 2
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 2
;; LENGTH: 277
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-270-478-2

Query Match 100.0%; Score 1528; DB 14; Length 277;
Best Local Similarity 100.0%; Pred. No. 6.7e-137;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GNONRFESLECKKCTRDNANRIIKTTLQOEKPDFCFLEEDPGICRGYITRYFYNNOTK 120
DB 62 GNONRFESLECKKCTRDNANRIIKTTLQOEKPDFCFLEEDPGICRGYITRYFYNNOTK 121

QY 121 QCFERFYGGCLGNMNFETLECKNICEDGPNQFQVDNYGTQLNANNSLTPQSTKVP 180
DB 122 QCFERFYGGCLGNMNFETLECKNICEDGPNQFQVDNYGTQLNANNSLTPQSTKVP 181

QY 181 FEHGPSWCLTPADRGGLCRANENRYNSVIGKCRPFKYSGCCGNNFTSKQECRLACK 240
DB 182 FEHGPSWCLTPADRGGLCRANENRYNSVIGKCRPFKYSGCCGNNFTSKQECRLACK 241

QY 241 KGFQIRISKGGLIKTKRKRKQKRVKIAVEEIFVKNM 276
DB 242 KGFQIRISKGGLIKTKRKRKQKRVKIAVEEIFVKNM 277

RESULT 8
US-10-270-479-2
;; Sequence 2, Application US/10270479
;; Publication No. US20030139340A1
;; GENERAL INFORMATION:
;; APPLICANT: Creasey, Abba
;; TITLE OF INVENTION: Treatment of Sepsis By Low-Dose
;; TITLE OF INVENTION: Administration of Tissue Factor Pathway Inhibitor (TFPI)
;; FILE REFERENCE: 012441.00026
;; CURRENT APPLICATION NUMBER: US/10/270,479
;; PRIOR FILING DATE: 2002-10-15
;; PRIOR APPLICATION NUMBER: US 60/328,806
;; PRIOR FILING DATE: 2001-10-15
;; NUMBER OF SEQ ID NOS: 2
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 2
;; LENGTH: 277
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-270-479-2

Query Match 100.0%; Score 1528; DB 14; Length 277;
Best Local Similarity 100.0%; Pred. No. 6.7e-137;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 2 DSEDEBHTIITDTELPPLKMHSCAFKADGPKAIMKRFNFITRQCEEFYGGCE 61

QY 61 GNONRFESLECKKCTRDNANRIIKTTLQOEKPDFCFLEEDPGICRGYITRYFYNNOTK 120
DB 62 GNONRFESLECKKCTRDNANRIIKTTLQOEKPDFCFLEEDPGICRGYITRYFYNNOTK 121

QY 121 QCFERFYGGCLGNMNFETLECKNICEDGPNQFQVDNYGTQLNANNSLTPQSTKVP 180
DB 122 QCFERFYGGCLGNMNFETLECKNICEDGPNQFQVDNYGTQLNANNSLTPQSTKVP 181

QY 181 FEHGPSWCLTPADRGGLCRANENRYNSVIGKCRPFKYSGCCGNNFTSKQECRLACK 240
DB 182 FEHGPSWCLTPADRGGLCRANENRYNSVIGKCRPFKYSGCCGNNFTSKQECRLACK 241

QY 241 KGFQIRISKGGLIKTKRKRKQKRVKIAVEEIFVKNM 276
DB 242 KGFQIRISKGGLIKTKRKRKQKRVKIAVEEIFVKNM 277

RESULT 9
US-10-167-351-1
;; Sequence 1, Application US/10167351
;; Publication No. US20030165896A1
;; GENERAL INFORMATION:
;; APPLICANT: DYAX CORP.
;; APPLICANT: Markland, William
;; APPLICANT: Ladner, Robert C.
;; TITLE OF INVENTION: Inhibitors of Human Plasmin Derived From The Kunitz Domains
;; FILE REFERENCE: DXX-007.2P US-4
;; CURRENT APPLICATION NUMBER: US/10/167,351
;; PRIOR FILING DATE: 2002-06-11
;; PRIOR APPLICATION NUMBER: 09/638,770
;; PRIOR FILING DATE: 2000-08-15
;; PRIOR APPLICATION NUMBER: 09/414,878
;; PRIOR FILING DATE: 1999-10-08
;; PRIOR APPLICATION NUMBER: 09/240,136

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; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 08/676,124
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: PCT/US95/00298
; PRIOR FILING DATE: 1995-01-11
; PRIOR APPLICATION NUMBER: 08/208,265
; PRIOR FILING DATE: 1994-03-10
; PRIOR APPLICATION NUMBER: 08/179,658
; PRIOR FILING DATE: 1994-01-11
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-167-351-1

Query Match          100.0%; Score 1528; DB 14; Length 304;
Best Local Similarity 100.0%; Pred. No. 7.5e-137;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 29 DSEDEEHTIITDELPLKLMHSCAFKADGPKCKAIAKRRFFNIFTRQCEEFYGGCE 88

Qy 61 GQNRFSLECKKCKCTRDNANRIIKTTLOQEKDFCFLEEDPGICRGYITRYFYNNQTK 120
Db 89 GQNRFSLECKKCKCTRDNANRIIKTTLOQEKDFCFLEEDPGICRGYITRYFYNNQTK 148

Qy 121 QCERFKYGGCLGNMNFETLECKNICEDGPNGFQVDNYGTQLNAVNNSLTPQSTKVPSSL 180
Db 149 QCERFKYGGCLGNMNFETLECKNICEDGPNGFQVDNYGTQLNAVNNSLTPQSTKVPSSL 208

Qy 181 FEHGPSWCLTPADRGLCRANENFYNSVIGKCRPFKYSGCGNENFTSKQECCLACK 240
Db 209 FEHGPSWCLTPADRGLCRANENFYNSVIGKCRPFKYSGCGNENFTSKQECCLACK 268

Qy 241 KGFIQRISKGLIKTKRKRKQKVIAEIEFVKNM 276
Db 269 KGFIQRISKGLIKTKRKRKQKVIAEIEFVKNM 304

; TITLE OF INVENTION: Production of Tissue Factor Pathway
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton St.
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/860,277
; FILING DATE: 04-Jun-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/639,273
; FILING DATE: 15-Aug-2000
; APPLICATION NUMBER: US/08/286,530
; FILING DATE: 05-Aug-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Saveriede, Paul B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0991.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-601-2585
; TELEFAX: 510-655-3542
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-860-277-2

Query Match          100.0%; Score 1528; DB 17; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.9e-137;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSEDEEHTIITDELPLKLMHSCAFKADGPKCKAIAKRRFFNIFTRQCEEFYGGCE 60
Db 77 DSEDEEHTIITDELPLKLMHSCAFKADGPKCKAIAKRRFFNIFTRQCEEFYGGCE 136

Qy 61 GQNRFSLECKKCKCTRDNANRIIKTTLOQEKDFCFLEEDPGICRGYITRYFYNNQTK 120
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Db 137 GQNRFPESLECKKMCCTRDNANRIKTTLQOEKPDFCFLEEDPGICRGYITRYFYNNQTK 196
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 Db 197 QCERFKYGGCLGNMNFETLECKNICEDGPNQFQVDNYGTOLNAVNNSLTPQSTKVPSSL 256
 QY 181 FEFHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFKYSGCGGNENFTSKOECLRACK 240
 Db 257 FEFHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFKYSGCGGNENFTSKOECLRACK 316
 QY 241 KGFQIRISKGGLIKTKRKRKQKRVKIAYEEIFVKNM 276
 Db 317 KGFQIRISKGGLIKTKRKRKQKRVKIAYEEIFVKNM 352

RESULT 12

US-09-741-106-9
 ; Sequence 9, Application US/09741106
 ; Publication No. US20020197667A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Innis, Michael
 ; Creasey, Abia
 ; TITLE OF INVENTION: Chimeric Proteins
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Chiron Corporation
 ; STREET: 4560 Horton St.
 ; CITY: Emeryville
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94608
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30B
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/741,106
 ; FILING DATE: 12-Dec-2000
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/286,521
 ; FILING DATE: 1994-08-05
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Saveriede, Paul B.
 ; REGISTRATION NUMBER: 36,914
 ; REFERENCE/DOCKET NUMBER: 0990.001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 510-601-2585
 ; TELEFAX: 510-655-3542
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 276 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Query Match 99.8%; Score 1525; DB 9; Length 276;
 Best Local Similarity 99.6%; Pred. No. 1.3e-136;
 Matches 275; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DSEDEEHTIITDTELPPLKLMHSFCFAKADGPGCKAIMKRFNFNITRQCEEFYGGCE 60
 Db 1 DSEDEEHTIITDTELPPLKLMHSFCFAKADGPGCKAIMKRFNFNITRQCEEFYGGCE 60
 QY 61 GQNRFPESLECKKMCCTRDNANRIKTTLQOEKPDFCFLEEDPGICRGYITRYFYNNQTK 120
 Db 61 GQNRFPESLECKKMCCTRDNANRIKTTLQOEKPDFCFLEEDPGICRGYITRYFYNNQTK 120

QY 121 QCERFKYGGCLGNMNFETLECKNICEDGPNQFQVDNYGTOLNAVNNSLTPQSTKVPSSL 180
 Db 121 QCERFKYGGCLGNMNFETLECKNICEDGPNQFQVDNYGTOLNAVNNSLTPQSTKVPSSL 180
 QY 181 FEFHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFKYSGCGGNENFTSKOECLRACK 240
 Db 181 FEFHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFKYSGCGGNENFTSKOECLRACK 240
 QY 241 KGFQIRISKGGLIKTKRKRKQKRVKIAYEEIFVKNM 276
 Db 241 KGFQIRISKGGLIKTKRKRKQKRVKIAYEEIFVKNM 276

RESULT 13

US-10-918-366-9
 ; Sequence 9, Application US/10918366
 ; Publication No. US20050008654A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Innis, Michael
 ; Creasey, Abia
 ; TITLE OF INVENTION: Chimeric Proteins
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Chiron Corporation
 ; STREET: 4560 Horton St.
 ; CITY: Emeryville
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94608
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30B
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/918,366
 ; FILING DATE: 16-Aug-2004
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/286,521
 ; FILING DATE: 05-AUG-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Saveriede, Paul B.
 ; REGISTRATION NUMBER: 36,914
 ; REFERENCE/DOCKET NUMBER: 0990.001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 510-601-2585
 ; TELEFAX: 510-655-3542
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 276 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Query Match 99.8%; Score 1525; DB 17; Length 276;
 Best Local Similarity 99.6%; Pred. No. 1.3e-136;
 Matches 275; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DSEDEEHTIITDTELPPLKLMHSFCFAKADGPGCKAIMKRFNFNITRQCEEFYGGCE 60
 Db 1 DSEDEEHTIITDTELPPLKLMHSFCFAKADGPGCKAIMKRFNFNITRQCEEFYGGCE 60
 QY 61 GQNRFPESLECKKMCCTRDNANRIKTTLQOEKPDFCFLEEDPGICRGYITRYFYNNQTK 120
 Db 61 GQNRFPESLECKKMCCTRDNANRIKTTLQOEKPDFCFLEEDPGICRGYITRYFYNNQTK 120
 QY 121 QCERFKYGGCLGNMNFETLECKNICEDGPNQFQVDNYGTOLNAVNNSLTPQSTKVPSSL 180
 Db 121 QCERFKYGGCLGNMNFETLECKNICEDGPNQFQVDNYGTOLNAVNNSLTPQSTKVPSSL 180

QY 181 FEFGPWSCLTPADRGCLCRANENRYNSVIGKCRPFKYSGCGGNNFTSKQECIRACK 240
DB 181 FEFGPWSCLTPADRGCLCRANENRYNSVIGKCRPFKYSGCGGNNFTSKQECIRACK 240
QY 241 KGFIORISGGLIKTKRKRKKQVRIAYEEIFVKNM 276
DB 241 KGFIORISGGLIKTKRKRKKQVRIAYEEIFVKNM 276

RESULT 14

US-10-860-277-3
; Sequence 3, Application US/10860277
; Publication No. US20050064556A1
; GENERAL INFORMATION:
; APPLICANT: Innes, Michael
; Creasey, Abia
; TITLE OF INVENTION: Production of Tissue Factor Pathway
; Inhibitor
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton St.
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/860,277
; FILING DATE: 04-Jun-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/639,273
; FILING DATE: 15-Aug-2000
; APPLICATION NUMBER: US/08/286,530
; FILING DATE: 05-Aug-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Savereide, Paul B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0991.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-601-2585
; TELEFAX: 510-655-3542
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 276 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-860-277-3

Query Match 99.8%; Score 1525; DB 17; Length 276;
Best Local Similarity 99.6%; Pred. No. 1.3e-136;
Matches 275; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 DSEDEEHTIITDLPPLKLMHSCAFKADGPGCKAIMKRPFFNIFTRQCEFIYGCCE 60
DB 1 DSEDEEHTIITDLPPLKLMHSCAFKADGPGCKAIMKRPFFNIFTRQCEFIYGCCE 60
QY 61 GNONRFESLECKKMKCTRDNANRIKTTLOQEKDPDFCFLEEDPGICRGYITRYFYNNQTK 120
DB 61 GNONRFESLECKKMKCTRDNANRIKTTLOQEKDPDFCFLEEDPGICRGYITRYFYNNQTK 120
QY 121 QCFERFKYGGCLGNMNFETLECKNICEDGPNFGVDNYGTQLNANVNSLTQSKTKVPSL 180
DB 121 QCFERFKYGGCLGNMNFETLECKNICEDGPNFGVDNYGTQLNANVNSLTQSKTKVPSL 180

QY 181 FEFGPWSCLTPADRGCLCRANENRYNSVIGKCRPFKYSGCGGNNFTSKQECIRACK 240
DB 181 FEFGPWSCLTPADRGCLCRANENRYNSVIGKCRPFKYSGCGGNNFTSKQECIRACK 240
QY 241 KGFIORISGGLIKTKRKRKKQVRIAYEEIFVKNM 276
DB 241 KGFIORISGGLIKTKRKRKKQVRIAYEEIFVKNM 276

RESULT 15

US-10-377-817-2
; Sequence 2, Application US/10377817
; Publication No. US20030166194A1
; GENERAL INFORMATION:
; APPLICANT: Broze, George J.
; Kretzmer, Kuniko K.
; APPLICANT: Wun, Tze-Chien
; TITLE OF INVENTION: Antibodies to human tissue factor
; TITLE OF INVENTION: inhibitor
; FILE REFERENCE: SM04941-10-US
; CURRENT APPLICATION NUMBER: US/10/377,817
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: US/09/627,676
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/054,782
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 08/463,323
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: 08/355,351
; PRIOR FILING DATE: 1993-07-15
; PRIOR APPLICATION NUMBER: 07/566,280
; PRIOR FILING DATE: 1990-08-13
; PRIOR APPLICATION NUMBER: 07/123,753
; PRIOR FILING DATE: 1987-11-23
; PRIOR APPLICATION NUMBER: 07/077,366
; PRIOR FILING DATE: 1987-07-23
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 304
; TYPE: PRT
; ORGANISM: human
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(29)
; OTHER INFORMATION: signal region
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (29)...(304)
; OTHER INFORMATION: mature protein
US-10-377-817-2

Query Match 99.6%; Score 1522; DB 14; Length 304;
Best Local Similarity 99.6%; Pred. No. 2.8e-136;
Matches 275; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 DSEDEEHTIITDLPPLKLMHSCAFKADGPGCKAIMKRPFFNIFTRQCEFIYGCCE 60
DB 29 DSEDEEHTIITDLPPLKLMHSCAFKADGPGCKAIMKRPFFNIFTRQCEFIYGCCE 88
QY 61 GNONRFESLECKKMKCTRDNANRIKTTLOQEKDPDFCFLEEDPGICRGYITRYFYNNQTK 120
DB 89 GNONRFESLECKKMKCTRDNANRIKTTLOQEKDPDFCFLEEDPGICRGYITRYFYNNQTK 148
QY 121 QCFERFKYGGCLGNMNFETLECKNICEDGPNFGVDNYGTQLNANVNSLTQSKTKVPSL 180
DB 149 QCFERFKYGGCLGNMNFETLECKNICEDGPNFGVDNYGTQLNANVNSLTQSKTKVPSL 208
QY 181 FEFGPWSCLTPADRGCLCRANENRYNSVIGKCRPFKYSGCGGNNFTSKQECIRACK 240
DB 209 FEFGPWSCLTPADRGCLCRANENRYNSVIGKCRPFKYSGCGGNNFTSKQECIRACK 268

Search completed: April 16, 2005, 03:40:57
Job time : 138 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 16, 2005, 03:15:48 ; Search time 173 Seconds
(Without alignments)
617.028 Million cell updates/sec

Title: US-10-753-079-1

Perfect score: 1528

Sequence: 1 DSEDEEHTITDTLPLK.....PKRKQKVIAIEIFVQNM 276

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1528	100.0	276	2 AAW30311	Aaw30311 Recombina
2	1528	100.0	276	2 AAW61535	Aaw61535 Human tis
3	1528	100.0	276	6 ABU07724	Abu07724 Human tis
4	1528	100.0	276	7 ADE80824	Ad80824 Human tis
5	1528	100.0	276	7 ADE80822	Ad80822 Human tis
6	1528	100.0	276	7 ADI20097	Adi20097 Human TFP
7	1528	100.0	276	8 ADQ76118	Adq76118 Human tis
8	1528	100.0	276	8 ADQ76119	Adq76119 Human tis
9	1528	100.0	277	7 ADE80825	Ad80825 Human tis
10	1528	100.0	277	7 ADE80823	Ad80823 Human tis
11	1528	100.0	277	7 ADI20098	Adi20098 Human Ala
12	1528	100.0	304	2 AAR67894	Aar67894 Tissue ra
13	1528	100.0	304	2 AAR81884	Aar81884 Lipoprote
14	1528	100.0	304	2 AAY49557	Aay49557 Human lip
15	1528	100.0	304	7 ADF09568	Adf09568 Human tis
16	1528	100.0	304	8 ADG88030	Adg88030 Human ser
17	1528	100.0	304	8 ADR14411	Adr14411 Human NF-
18	1528	100.0	352	2 AAR92011	Aar92011 Ubiquitin
19	1525	99.8	276	2 AAR92012	Aar92012 TFP mute
20	1525	99.8	276	2 AAR92265	Aar92265 TFP mute
21	1522	99.6	304	3 AAY92002	Aay92002 Human tis
22	1517	99.3	304	3 AAY70273	Aay70273 Human tis
23	1514	99.1	304	2 AAR78389	Aar78389 Human lip
24	1512	98.0	277	2 AAR37312	Aar37312 Non-glyco
25	1507	98.6	304	3 AAY70272	Aay70272 Human mut

26	1502.5	98.3	327	8 ABM83494	Abm83494 Human dia
27	1447.5	94.7	291	6 ABR48476	AbR48476 Human Tif
28	1447	94.7	304	2 AAR42309	Aar42309 LACI gene
29	1446	94.6	265	2 AAR11170	Aar11170 Ser-(Aspl
30	1444.5	94.5	291	6 ABR48478	AbR48478 Human Tif
31	1428.5	93.5	262	2 AAR11172	Aar11172 Ser-(Aspl
32	1422	93.1	261	2 AAR11171	Aar11171 Ser-(Aspl
33	1417	92.7	256	2 AAR11169	Aar11169 Ser-(Aspl-
34	1005	65.8	225	4 AAU02971	Aau02971 Angiotens
35	979.5	64.1	274	8 ABM83495	Abm83495 Human dia
36	934.5	61.2	302	2 AAR35001	Aar35001 LACI, 7/1
37	934.5	61.2	302	2 AAR88513	Aar88513 Lipoprote
38	901	59.0	160	2 AAR23800	Aar23800 LACI frag
39	894	58.5	161	2 AAW00017	Aaw00017 TFPI chim
40	888	58.1	189	2 AAR11167	Aar11167 (Aspl)-thr
41	834	54.6	183	2 AAR11146	Aar11146 Ser-(Glul
42	797	52.2	459	8 ADG74024	Adg74024 Annexin V
43	745	48.8	164	6 ABR48500	AbR48500 Human Tis
44	679	44.4	161	4 AAU02982	Aau02982 Angiotens
45	660	43.2	152	6 ABR48499	AbR48499 Human Tis

ALIGNMENTS

RESULT 1

AAW30311
ID AAW30311 standard; protein; 276 AA.

XX AAW30311;

XX 30-JAN-1998 (first entry)

DE Recombinant non-glycosylated TFPI.

XX Tissue factor pathway inhibitor; TFPI; human; tissue factor inhibitor;

KW Lipoprotein-associated coagulation inhibitor; coagulation inhibitor; TFI;
KW LACI; extrinsic pathway inhibitor; protein refolding; clot-inhibitor;
KW protein solubility modification; EPI.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 2 /note= "phosphorylated to varying degrees, but does not
FT affect TFPI function"

FT Disulfide-bond 26..76

FT Disulfide-bond 35..59

FT Disulfide-bond 51..72

FT Disulfide-bond 97..147

FT Disulfide-bond 106..130

FT Disulfide-bond 122..143

FT Disulfide-bond 189..239

FT Disulfide-bond 198..222

FT Disulfide-bond 214..235

XX WO9640784-A2.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US009980.

XX 07-JUN-1995; 95US-00473668.

XX 07-JUN-1995; 95US-00477677.

XX (CHIR) CHIRON CORP.

XX (SEAR) SEARLE & CO G D.

XX Dorin GJ, Arve BH, Pattison GL, Hallenbeck RF, Johnson K, Chen B;

XX Rana RK, Hora MS, Madani H, Gustafson ME, Tsang M, Bild GS;

XX Johnson GV;

XX WPI; 1997-087056/08.

XX Aq. formulation of tissue factor pathway inhibitor - contains charged
PT polymer, e.g. dextran sulphate, to facilitate solubilisation, formulation
XT purification and refolding of protein.
PS Disclosure; Fig 4; 86pp; English.

XX This sequence represents the human tissue factor pathway inhibitor (TFPI)
CC protein. TFPI is also known as Lipoprotein-associated coagulation
CC inhibitor (LACI), extrinsic pathway inhibitor (EPI) and tissue factor
CC inhibitor (TFI). The DNA encoding this sequence was altered to contain
CC the optimum codons for expression in E. coli, to allow for expression of
CC this protein in the bacteria. TFPI is used in the aqueous formulation of
CC the invention. The aqueous formulation also includes a charged polymer
CC (CP), preferably a sulphated polysaccharide (such as heparin or dextran
CC sulphate) or a polyphosphate, preferably immobilised on a solid support.
CC The CP is added to aid the correct refolding of TFPI. TFPI can also be
CC modified or refolded using the methods of the invention. One method is
CC for modifying the solubility of a protein, by adding an aqueous solution
CC of a CP to reduce inter- and intra-molecular interactions between the
CC charged domains of the protein. The second method is for refolding an
CC improperly folded or denatured protein (e.g. TFPI), and comprises adding
CC CP to a solution of the protein prior to allowing the protein to refold.
CC The methods are particularly useful for solubilising, formulating,
CC purifying and refolding proteins (especially TFPI) which have been
CC engineered by genetic recombination and produced in bacterial, yeast or
CC other cells in a form that has a non-native tertiary structure. TFPI is a
CC coagulation inhibitor which has clot-inhibiting properties
XX Sequence 276 AA;

Query Match 100.0%; Score 1528; DB 2; Length 276;
Best Local Similarity 100.0%; Pred. No. 1.2e-129;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DSEDEEHTIITDELPLPLKMHSCAFKADGPKAKMKRFFNITROCEEFYGGCE 60
DB 1 DSEDEEHTIITDELPLPLKMHSCAFKADGPKAKMKRFFNITROCEEFYGGCE 60
QY 61 GNQNFESLECKKMCCTRDNANRIKTTLOQEKPDFCFLEEDPGICRGYITRYFYNNQTK 120
DB 61 GNQNFESLECKKMCCTRDNANRIKTTLOQEKPDFCFLEEDPGICRGYITRYFYNNQTK 120
QY 121 QCRFYKGGCLGNMNPETLECKNICEDGPNQFQVDNYGTOLNANNSLTPQSTKVPSSL 180
DB 121 QCRFYKGGCLGNMNPETLECKNICEDGPNQFQVDNYGTOLNANNSLTPQSTKVPSSL 180
QY 181 FEFHGPSWCLTPADRGICRANENRFYNSVIGKCRPFKYSGCGGNNFTSKQECRLACK 240
DB 181 FEFHGPSWCLTPADRGICRANENRFYNSVIGKCRPFKYSGCGGNNFTSKQECRLACK 240
QY 241 KGFIQIRISKGLIKTKRKQRKQVIAEYEIFVKNM 276
DB 241 KGFIQIRISKGLIKTKRKQRKQVIAEYEIFVKNM 276

RESULT 2
AAW61535
ID AAW61535 standard; protein; 276 AA.
AC AAW61535;
XX
DT 06-NOV-1998 (first entry)
DE Human tissue factor pathway inhibitor (TFPI).
XX Human tissue factor pathway inhibitor; TFPI; TFPI-2; cell proliferation;
KW angiogenesis-related disease; cancer; arthritis; macular degeneration;
KW diabetic retinopathy.
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers

FT Modified-site 2
FT Domain /note= "Potential phosphorylation site"
FT 26..76
FT Disulfide-bond /note= "Kunitz-1 type protease inhibitor domain"
FT 26..76
FT Disulfide-bond 35..59
FT Disulfide-bond 51..72
FT Domain 97..147
FT /note= "Kunitz-2 type protease inhibitor domain"
FT Disulfide-bond 97..147
FT Disulfide-bond 106..130
FT Modified-site 117
FT /note= "N-glycosylated"
FT Disulfide-bond 122..143
FT Modified-site 167
FT /note= "N-glycosylated"
FT Domain 189..239
FT /note= "Kunitz-3 type protease inhibitor domain"
FT Disulfide-bond 189..239
FT Disulfide-bond 198..222
FT Disulfide-bond 214..235
FT Modified-site 228
FT /note= "N-glycosylated"
XX WO9834634-A1.
PN 13-AUG-1998.
PD
XX 06-FEB-1998; 98WO-US002699.
XX 06-FEB-1997; 97US-00796850.
PA (ENTR-) ENTREMED INC.
XX Papathanassiou AE, Green SJ;
XX WPI; 1998-446947/38.
XX Composition comprising tissue factor pathway inhibitor for inhibiting
PT cell proliferation - for treating angiogenesis related diseases e.g.
PT cancer, arthritis, macular degeneration and diabetic retinopathy.
XX Claim 6; Page 23-24; 37pp; English.

XX The present sequence represents the human tissue factor pathway inhibitor
CC (TFPI). The invention provides compositions using TFPI and its homologs,
CC e.g. TFPI-2 (AAW61536), for inhibiting cell proliferation. The
CC compositions are claimed to be useful for inhibiting an angiogenesis-
CC related disease, such as cancer, arthritis, macular degeneration or
CC diabetic retinopathy
XX Sequence 276 AA;

Query Match 100.0%; Score 1528; DB 2; Length 276;
Best Local Similarity 100.0%; Pred. No. 1.2e-129;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DSEDEEHTIITDELPLPLKMHSCAFKADGPKAKMKRFFNITROCEEFYGGCE 60
DB 1 DSEDEEHTIITDELPLPLKMHSCAFKADGPKAKMKRFFNITROCEEFYGGCE 60
QY 61 GNQNFESLECKKMCCTRDNANRIKTTLOQEKPDFCFLEEDPGICRGYITRYFYNNQTK 120
DB 61 GNQNFESLECKKMCCTRDNANRIKTTLOQEKPDFCFLEEDPGICRGYITRYFYNNQTK 120
QY 121 QCRFYKGGCLGNMNPETLECKNICEDGPNQFQVDNYGTOLNANNSLTPQSTKVPSSL 180
DB 121 QCRFYKGGCLGNMNPETLECKNICEDGPNQFQVDNYGTOLNANNSLTPQSTKVPSSL 180
QY 181 FEFHGPSWCLTPADRGICRANENRFYNSVIGKCRPFKYSGCGGNNFTSKQECRLACK 240
DB 181 FEFHGPSWCLTPADRGICRANENRFYNSVIGKCRPFKYSGCGGNNFTSKQECRLACK 240

QY 241 KGFQRIKSGGLIKTKRKKRQVIAVEEIVKNN 276
Db |||||

RESULT 3

ABU07724
ID ABU07724 standard; protein; 276 AA.

XX AC ABU07724;

XX DT 28-MAY-2003 (first entry)

XX DE Human tissue factor pathway inhibitor-1, TPPI-1.

XX Human; TPPI-1; tissue factor pathway inhibitor-1; telangiectasia; LACI;
KW endothelial cell proliferation; proteinase inhibitor; angiogenesis;
KW lipoprotein-associated coagulation inhibitor; haemangioma; solid tumour;
KW leukaemia; metastasis; psoriasis; scleroderma; pyogenic granuloma;
KW myocardial angiogenesis; plaque neovascularisation; coronary collateral;
KW ischaemic limb angiogenesis; corneal disease; rubecosis; arthritis;
KW neovascular glaucoma; diabetic retinopathy; retrolental fibroplasia;
KW diabetic neovascularisation; macular degeneration; wound healing;
KW peptic ulcer; fracture; vasculogenesis; haematopoiesis; ovulation;
KW keloid; menstruation; placentation.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Domain 26..76 /note= "Kunitz-1 domain"

FT Disulfide-bond 26..76

FT Disulfide-bond 35..59

FT Disulfide-bond 51..72

FT Domain 97..147 /note= "Kunitz-2 domain"

FT Disulfide-bond 97..147

FT Disulfide-bond 106..130

FT Modified-site 117.. /note= "N-glycosylated"

FT Disulfide-bond 122..143

FT Modified-site 167 /note= "N-glycosylated"

FT Domain 189..239 /note= "Kunitz-3 domain"

FT Disulfide-bond 189..239

FT Disulfide-bond 198..222

FT Disulfide-bond 214..235

FT Modified-site 228 /note= "N-glycosylated"

FT Region 232..276

FT /note= "Region described as SEQ ID NO:1 specifically
claimed in claim 6"

FT Region 247..276

FT /note= "Region described as SEQ ID NO:2 specifically
claimed in claim 6"

FT Region 254..276

FT /note= "Region described as SEQ ID NO:3 specifically
claimed in claim 6"

FT FT

XX US2002173465-A1.

XX PD 21-NOV-2002.

XX PF 28-FEB-2002; 2002US-00086176.

XX PR 06-FEB-1997; 97US-00796850.

PR 06-AUG-1998; 98US-00130273.

PR 11-JAN-1999; 99US-0027955.

PR 22-JAN-2001; 2001US-00766778.

XX (HEMB/) HEMBROUGH T.

PA (PRIB/) PRIBLUDA V P.

PA (PAPA/) PAPATHANASSIU A E.
XX (GREE/) GREEN S J.

XX Hembrough T, Pribluda VP, Papathanassiu AE, Green SJ;

XX WPI; 2003-311004/30.

XX Treating a human or animal with undesirable endothelial cell

PT proliferation, e.g. solid tumors, leukemia, metastasis, corneal diseases
PT by administering a composition comprising a tissue factor pathway
PT inhibitor C-terminal peptide.

XX Claim 5; Fig 1; 28pp; English.

CC The invention relates to a method of treating a human or animal with
CC undesirable endothelial cell proliferation which comprises administering
CC a composition comprising a tissue factor pathway inhibitor (TFPI) C-
CC terminal peptide to inhibit the undesirable endothelial cell
CC proliferation. TFPI also known as lipoprotein-associated coagulation
CC inhibitor (LACI) is a proteinase inhibitor. The method is useful for
CC treating undesirable endothelial cell proliferation, specifically an
CC angiogenesis-related disease, such as haemangioma, solid tumours,
CC leukaemia, metastasis, telangiectasia, psoriasis, scleroderma, pyogenic
CC granuloma, myocardial angiogenesis, plaque neovascularisation, coronary
CC collateral, ischaemic limb angiogenesis, corneal diseases, rubecosis,
CC neovascular glaucoma, diabetic retinopathy, retrolental fibroplasias,
CC arthritis, diabetic neovascularisation, macular degeneration, wound
CC healing, peptic ulcer, fractures, keloids, vasculogenesis,
CC haematopoiesis, ovulation, menstruation or placentation. The present
CC sequence represents the amino acid sequence of human tissue factor
CC pathway inhibitor-1, TPPI-1

XX Sequence 276 AA;

Query Match 100.0%; Score 1528; DB 6; Length 276;

Best Local Similarity 100.0%; Pred. No. 1.2e-129;

Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEHTIITDELPLPLKMHSPCAFADGPKADGPKAIMKGFFFNFTQCSEFIYGGCE 60

Db 1 DSEDEHTIITDELPLPLKMHSPCAFADGPKADGPKAIMKGFFFNFTQCSEFIYGGCE 60

QY 61 GNQRFESLEECKKMCCTRDNANRIKTTLOQEKDFCFLEEDPGICRGVITRYFYNNQTK 120

Db 61 GNQRFESLEECKKMCCTRDNANRIKTTLOQEKDFCFLEEDPGICRGVITRYFYNNQTK 120

QY 121 QCERFKYGGCLGNMNNFETLECKNICEDGPNQFVDNYGTQLNANNSLTPQSTKVPSL 180

Db 121 QCERFKYGGCLGNMNNFETLECKNICEDGPNQFVDNYGTQLNANNSLTPQSTKVPSL 180

QY 181 FEFGPSWCLTPADRGLCRANENFYNSVIGKCRPPFKYSGCGGNENFTSKQECIRACK 240

Db 181 FEFGPSWCLTPADRGLCRANENFYNSVIGKCRPPFKYSGCGGNENFTSKQECIRACK 240

QY 241 KGFTQRIKSGGLIKTKRKKRQVIAVEEIVKNN 276

Db 241 KGFTQRIKSGGLIKTKRKKRQVIAVEEIVKNN 276

RESULT 4

ADE80824

ID ADE80824 standard; protein; 276 AA.

XX AC ADE80824;

XX DT 29-JAN-2004 (first entry)

XX Human tissue factor pathway inhibitor (TFPI) protein.

DE Severe pneumonia; tissue factor pathway inhibitor; TPPI; N-L-alanyl-L-TPPI;

XX ala-TPPI; Kunitz domain; human ; antiinflammatory.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 XX FT Domain 19..89
 XX FT /label = Kunitz domain
 XX FT /note= "Specifically claimed in Claim 18"
 XX FT Domain 90..160
 XX FT /label = Kunitz domain
 XX FT /note= "Specifically claimed in Claim 19 and Claim 21"
 XX PN US2003139339-A1.
 XX PD 24-JUL-2003.
 XX PF 15-OCT-2002; 2002US-00270478.
 XX PR 15-OCT-2001; 2001US-0328806P.
 XX PA (CREA/) CREASEY A.
 XX PI Creasey A;
 XX DR WPI; 2003-897354/82.
 XX PT Treating or preventing severe pneumonia by administering tissue factor
 PT pathway inhibitor (TFPI) or its analog to a patient having or is at risk
 PT of having severe pneumonia.
 XX PS Claim 20; SEQ ID NO 1; 14pp; English.
 XX CC The present invention relates to a method for treating or preventing
 CC severe pneumonia. The method comprises administering tissue factor
 CC pathway inhibitor (TFPI) or its analogue to a patient having, or at risk
 CC of having severe pneumonia. The method involves the use of continuous
 CC intravenous infusion of TFPI or TFPI analogue, preferably at low doses to
 CC avoid adverse side effects. The TFPI analogue is non-glycosylated N-L-
 CC alanyl-TFPI (ala-TFPI). It comprises a first or second Kunitz domain. The
 CC method is useful for treating or preventing severe pneumonia. The present
 CC sequence represents human TFPI protein.
 XX SQ Sequence 276 AA;
 Query Match 100.0%; Score 1528; DB 7; Length 276;
 Best Local Similarity 100.0%; Pred. No. 1.2e-129;
 Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DSEDEEHTIITDTELPPLKLMHSFCAPKADGPKAIIKRRFFNFITRQCEEFYGGCE 60
 Db 1 DSEDEEHTIITDTELPPLKLMHSFCAPKADGPKAIIKRRFFNFITRQCEEFYGGCE 60
 QY 61 GNONRFESLECKKMCCTRDNANRIITLQEKPDPCFLEEDPGICRGYITRYFNNQTK 120
 Db 61 GNONRFESLECKKMCCTRDNANRIITLQEKPDPCFLEEDPGICRGYITRYFNNQTK 120
 QY 121 QCFERFYGGCLGNMNFETLECKNICEDGPGFQVDNYGTQLNAVNNSLTPQSTKVP 180
 Db 121 QCFERFYGGCLGNMNFETLECKNICEDGPGFQVDNYGTQLNAVNNSLTPQSTKVP 180
 QY 181 FEHGPSWCLTPADRGLCRANENRFYNSVIGKCRPFKYSKCGGNNNFITSKQEC 240
 Db 181 FEHGPSWCLTPADRGLCRANENRFYNSVIGKCRPFKYSKCGGNNNFITSKQEC 240
 QY 241 KGFIQRISKGLIKTKRKRKQKVIAEIEIFVKNM 276
 Db 241 KGFIQRISKGLIKTKRKRKQKVIAEIEIFVKNM 276
 RESULT 5
 ADE80822
 ID ADE80822 standard; protein; 276 AA.
 XX AC ADE80822;
 XX DT 29-JAN-2004 (first entry)

XX Human tissue factor pathway inhibitor (TFPI) protein.
 XX DE 19..89
 XX KW Sepsis; septic shock; tissue factor pathway inhibitor; TFPI;
 KW N-L-alanyl-TFPI; ala-TFPI; Kunitz domain; human; antibacterial;
 KW antiinflammatory.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX FT Domain 19..89
 XX FT /label = Kunitz domain
 XX FT /note= "Specifically claimed in Claim 3"
 XX FT Domain 90..160
 XX FT /label = Kunitz domain
 XX FT /note= "Specifically claimed in Claim 4 and Claim 6"
 XX PN US2003139340-A1.
 XX PD 24-JUL-2003.
 XX PF 04-FEB-2003; 2003US-00270479.
 XX PR 15-OCT-2001; 2001US-0328806P.
 XX PA (CREA/) CREASEY A.
 XX PI Creasey A;
 XX DR WPI; 2003-897355/82.
 XX PT Treating sepsis by administering TFPI or its analog by continuous
 PT intravenous infusion at dose rate equivalent to reference ala-TFPI at
 PT dose rate of less than 0.00025-0.050 mg/hr for at least 72 hours.
 XX PS Claim 5; SEQ ID NO 1; 27pp; English.
 XX CC The present invention relates to a method for treating or preventing
 CC sepsis or septic shock. The method comprises administering tissue factor
 CC pathway inhibitor (TFPI) or its analogue to a patient having, or at risk
 CC of having sepsis or septic shock. The method involves the use of
 CC continuous intravenous infusion of TFPI or TFPI analogue, preferably at
 CC low doses to avoid adverse side effects. The TFPI analogue is non-
 CC glycosylated N-L-alanyl-TFPI (ala-TFPI). It comprises a first or second
 CC Kunitz domain. The method is useful for treating or preventing sepsis or
 CC septic shock. The present sequence represents human TFPI protein.
 XX SQ Sequence 276 AA;
 Query Match 100.0%; Score 1528; DB 7; Length 276;
 Best Local Similarity 100.0%; Pred. No. 1.2e-129;
 Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DSEDEEHTIITDTELPPLKLMHSFCAPKADGPKAIIKRRFFNFITRQCEEFYGGCE 60
 Db 1 DSEDEEHTIITDTELPPLKLMHSFCAPKADGPKAIIKRRFFNFITRQCEEFYGGCE 60
 QY 61 GNONRFESLECKKMCCTRDNANRIITLQEKPDPCFLEEDPGICRGYITRYFNNQTK 120
 Db 61 GNONRFESLECKKMCCTRDNANRIITLQEKPDPCFLEEDPGICRGYITRYFNNQTK 120
 QY 121 QCFERFYGGCLGNMNFETLECKNICEDGPGFQVDNYGTQLNAVNNSLTPQSTKVP 180
 Db 121 QCFERFYGGCLGNMNFETLECKNICEDGPGFQVDNYGTQLNAVNNSLTPQSTKVP 180
 QY 181 FEHGPSWCLTPADRGLCRANENRFYNSVIGKCRPFKYSKCGGNNNFITSKQEC 240
 Db 181 FEHGPSWCLTPADRGLCRANENRFYNSVIGKCRPFKYSKCGGNNNFITSKQEC 240
 QY 241 KGFIQRISKGLIKTKRKRKQKVIAEIEIFVKNM 276
 Db 241 KGFIQRISKGLIKTKRKRKQKVIAEIEIFVKNM 276

QY 241 KGFIQRISKGLIKTKRKRKKQVVKIAYEEIFVKNM 276
DB 241 KGFIQRISKGLIKTKRKRKKQVVKIAYEEIFVKNM 276

RESULT 8
ID ADQ76119
AC ADQ76119 standard; protein; 276 AA.
XX ADQ76119;
DT 21-OCT-2004 (first entry)
DE Human tissue factor pathway inhibitor protein.
KW Aqueous composition; aggregation stability; oxidation;
KW tissue factor pathway inhibitor; TFPI; solubilising agent; antioxidant;
KW antibacterial; immunosuppressive; thrombolytic; vasotropic; cytostatic;
KW sepsis; deep vein thrombosis; ischaemia; restenosis; cancer; unfolding;
KW refolding; denaturation; human.
XX Homo sapiens.
OS
XX
XX WO2004062689-A1.
XX
XX 29-JUL-2004.
XX
XX 08-JAN-2004; 2004WO-US000233.
XX
XX 08-JAN-2003; 2003US-0438519P.
XX 13-AUG-2003; 2003US-0494577P.
XX 08-OCT-2003; 2003US-0509260P.
XX 20-OCT-2003; 2003US-0512090P.
XX
XX (CHIR) CHIRON CORP.
XX
XX Chen B;
XX
XX WPI; 2004-561766/54.
XX
XX Aqueous composition, useful to treat e.g. deep vein thrombosis, sepsis
XX and cancer, comprises tissue factor pathway inhibitor or its variant, a
XX solubilizing agent (e.g. arginine) and an antioxidant (e.g. an oxygen
XX displacing gas).
XX
XX Claim 2; SEQ ID NO 1; 55pp; English.
XX
XX The invention relates to a novel aqueous composition (having 45% or more
XX aggregation stability, 45% or more oxidation stability and 4-8 pH). The
XX composition comprises 0.05-15 mg/ml of a tissue factor pathway inhibitor
XX (TFPI) or its variant, 50-600 mM of a solubilising agent (arginine or its
XX analogue and/or lysine or its analogue) and an antioxidant (an oxygen
XX displacing gas, an oxygen or free radical scavenger and/or a chelating
XX agent). The invention further comprises a pharmaceutical composition
XX comprising the aqueous composition. The aqueous composition has the
XX following activities: antibacterial, immunosuppressive, thrombolytic,
XX vasotropic, and cytostatic. The aqueous solution is useful to treat
XX sepsis, deep vein thrombosis, ischaemia, restenosis and cancer. The use
XX of a solubilising agent and an oxidant improves the stability of the
XX aqueous compositions comprising TFPI or its variant. The aqueous
XX compositions also resist other detrimental effects (e.g. unfolding,
XX refolding and denaturation) that results in a loss of biological activity
XX or in undesirable characteristics. This sequence represents a human
XX tissue factor pathway inhibitor protein of the invention.
XX
XX Sequence 276 AA;

Query Match 100.0%; Score 1528; DB 8; Length 276;
Best Local Similarity 100.0%; Pred. No. 1.2e-129;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEHIIITDELPLKLMHSFCAPKADGPKCAIMKRFNFIPTROCEFIYGGCE 60
DB 1 DSEDEHIIITDELPLKLMHSFCAPKADGPKCAIMKRFNFIPTROCEFIYGGCE 60

QY 241 KGFIQRISKGLIKTKRKRKKQVVKIAYEEIFVKNM 276
DB 241 KGFIQRISKGLIKTKRKRKKQVVKIAYEEIFVKNM 276

RESULT 9
ID ADE80825 standard; protein; 277 AA.
XX ADE80825;
AC ADE80825;
XX
XX 29-JAN-2004 (first entry)
XX
XX Human tissue factor pathway inhibitor (TFPI) analogue, ala-TFPI.
XX
XX Severe pneumonia; tissue factor pathway inhibitor; TFPI; N-L-alanyl-TFPI;
XX ala-TFPI; TFPI analogue; Kunitz domain; human; antiinflammatory.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX US2003139339-A1.
XX
XX 24-JUL-2003.
XX
XX 15-OCT-2002; 2002US-00270478.
XX
XX 15-OCT-2001; 2001US-0328806P.
XX
XX (CREA/) CREASEY A.
XX
XX Creasey A;
XX
XX WPI; 2003-897354/82.
XX
XX Treating or preventing severe pneumonia by administering tissue factor
XX pathway inhibitor (TFPI) or its analogue to a patient having, or at risk
XX of having severe pneumonia. The method involves the use of continuous
XX intravenous infusion of TFPI or TFPI analogue, preferably at low doses to
XX avoid adverse side effects. The TFPI analogue is non-glycosylated N-L-
XX alanyl-TFPI (ala-TFPI). It comprises a first or second Kunitz domain. The
XX method is useful for treating or preventing severe pneumonia. The present
XX sequence represents human TFPI analogue, ala-TFPI.
XX
XX Sequence 277 AA;

Query Match 100.0%; Score 1528; DB 7; Length 277;
Best Local Similarity 100.0%; Pred. No. 1.2e-129;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEHIIITDELPLKLMHSFCAPKADGPKCAIMKRFNFIPTROCEFIYGGCE 60
DB 1 DSEDEHIIITDELPLKLMHSFCAPKADGPKCAIMKRFNFIPTROCEFIYGGCE 60

Db 2 DSEDEEHTIITDTELPLPLKMHSCAFKADDPCKAIMKRRFFNIFTRQCEEFYGGCE 61
 Qy 61 GNQRFESLECKKMCCTRDNANRIKTTLQEKDPDFCFLEEDPGICRGYITRYFYNNQTK 120
 Db 62 GNQRFESLECKKMCCTRDNANRIKTTLQEKDPDFCFLEEDPGICRGYITRYFYNNQTK 121
 Qy 121 QCERFKYGGCLGNMNNFETLECKNICEDGPNQGVNDYGTQLNAVNNSLTPQSTKVPSSL 180
 Db 122 QCERFKYGGCLGNMNNFETLECKNICEDGPNQGVNDYGTQLNAVNNSLTPQSTKVPSSL 181
 Qy 181 FEFHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFKYSGCGNENFTSKQECCLACK 240
 Db 182 FEFHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFKYSGCGNENFTSKQECCLACK 241
 Qy 241 KGFIQIRISKGLIKTKRKRKQVVKIAYEEIFVKNM 276
 Db 242 KGFIQIRISKGLIKTKRKRKQVVKIAYEEIFVKNM 277

RESULT 10

ADE80823
 ID ADE80823 standard; protein; 277 AA.

AC ADE80823;

DT 29-JAN-2004 (first entry)

XX Human tissue factor pathway inhibitor (TFPI) analogue, ala-TFPI.

DE Sepsis; septic shock; tissue factor pathway inhibitor; TFPI;

KW N-L-alanyl-TFPI; ala-TFPI; TFPI analogue; Kunitz domain; human;

KW antibacterial; antiinflammatory.

OS Synthetic.

OS Homo sapiens.

XX US2003139340-A1.

PN 24-JUL-2003.

PD 04-FEB-2003; 2003US-00270479.

PF 15-OCT-2001; 2001US-0328806P.

PR (CREA/) CREASEY A.

XX Creasey A;

XX WPI; 2003-897355/82.

XX Treating sepsis by administering TFPI or its analog by continuous
 PT intravenous infusion at dose rate equivalent to reference ala-TFPI at
 PT dose rate of less than 0.0025-0.050 mg/kg/hr for at least 72 hours.

XX Disclosure; SEQ ID NO 2; 277p; English.

XX The present invention relates to a method for treating or preventing
 CC sepsis or septic shock. The method comprises administering tissue factor
 CC pathway inhibitor (TFPI) or its analogue to a patient having, or at risk
 CC of having sepsis or septic shock. The method involves the use of
 CC continuous intravenous infusion of TFPI or TFPI analogue, preferably at
 CC low doses to avoid adverse side effects. The TFPI analogue is non-
 CC glycosylated N-L-alanyl-TFPI (ala-TFPI). It comprises a first or second
 CC Kunitz domain. The method is useful for treating or preventing sepsis or
 CC septic shock. The present sequence represents human TFPI analogue, ala-
 CC TFPI.

XX Sequence 277 AA;

Query Match 100.0%; Score 1528; DB 7; Length 277;

Best Local Similarity 100.0%; Pred. No. 1.2e-129;

Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSEDEEHTIITDTELPLPLKMHSCAFKADDPCKAIMKRRFFNIFTRQCEEFYGGCE 60
 Db 2 DSEDEEHTIITDTELPLPLKMHSCAFKADDPCKAIMKRRFFNIFTRQCEEFYGGCE 61
 Qy 61 GNQRFESLECKKMCCTRDNANRIKTTLQEKDPDFCFLEEDPGICRGYITRYFYNNQTK 120
 Db 62 GNQRFESLECKKMCCTRDNANRIKTTLQEKDPDFCFLEEDPGICRGYITRYFYNNQTK 121
 Qy 121 QCERFKYGGCLGNMNNFETLECKNICEDGPNQGVNDYGTQLNAVNNSLTPQSTKVPSSL 180
 Db 122 QCERFKYGGCLGNMNNFETLECKNICEDGPNQGVNDYGTQLNAVNNSLTPQSTKVPSSL 181
 Qy 181 FEFHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFKYSGCGNENFTSKQECCLACK 240
 Db 182 FEFHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFKYSGCGNENFTSKQECCLACK 241
 Qy 241 KGFIQIRISKGLIKTKRKRKQVVKIAYEEIFVKNM 276
 Db 242 KGFIQIRISKGLIKTKRKRKQVVKIAYEEIFVKNM 277

RESULT 11

ADI20098

ID ADI20098 standard; protein; 277 AA.

AC ADI20098;

DT 22-APR-2004 (first entry)

XX Human Ala-TFPI analog.

DE tissue factor pathway inhibitor; TFPI; Antibacterial; Immunosuppressive;

KW Antiinflammatory; chronic inflammation; sepsis; shock;

KW acute respiratory distress syndrome; ARDS.

XX Homo sapiens.

XX WO2003055442-A2.

PN 10-JUL-2003.

PD 15-OCT-2002; 2002WO-US032625.

PF 15-OCT-2001; 2001US-0328806P.

PR (CHIR) CHIRON CORP.

XX Creasey AA;

XX WPI; 2003-902653/82.

XX Treating sepsis involves continuous intravenous infusion of tissue factor
 PT pathway inhibitor or tissue factor pathway inhibitor analog to a patient.

XX Disclosure; SEQ ID NO 2; 589p; English.

XX The present invention relates to treating sepsis comprising continuous
 CC intravenous infusion of tissue factor pathway inhibitor (TFPI) or TFPI
 CC analog to a patient at a dose rate equivalent to administration of
 CC reference ala-TFPI. The method is useful for treating a patient suffering
 CC from sepsis, shock, or acute respiratory distress syndrome (ARDS), is
 CC useful for treating acute inflammation and for treating chronic or acute
 CC inflammation. The present sequence represents human Ala-TFPI analog.

XX Sequence 277 AA;

Query Match 100.0%; Score 1528; DB 7; Length 277;

Best Local Similarity 100.0%; Pred. No. 1.2e-129;

Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSEDEEHTIITDTELPLPLKMHSCAFKADDPCKAIMKRRFFNIFTRQCEEFYGGCE 60

Db 2 DSEDEEHTIITDTELPLPLKMHSCAFKADDPCKAIMKRRFFNIFTRQCEEFYGGCE 61


```
QY 61 GNQRFESLECKKQCTRDNANRIIKTTLQOEKDPDFCFLEEDPGICRGYITRYFYNNQTK 120
Db 62 GNQRFESLECKKQCTRDNANRIIKTTLQOEKDPDFCFLEEDPGICRGYITRYFYNNQTK 121
QY 121 QCERFKYGGCLGNMNFETLECKNICEDGPNQFQVDNYGTQLNAVNNSLTPQSTKVPSSL 180
Db 122 QCERFKYGGCLGNMNFETLECKNICEDGPNQFQVDNYGTQLNAVNNSLTPQSTKVPSSL 181
QY 181 FEFHGPSWCLTPADRGGLCRANENRFFYNSVIGKCRPFKYSGCGGNENFTSKQECIRACK 240
Db 182 FEFHGPSWCLTPADRGGLCRANENRFFYNSVIGKCRPFKYSGCGGNENFTSKQECIRACK 241
QY 241 KGFIQIRISKGGLIKTKRKRKQKRVKIAYEEIFVKNM 276
Db 242 KGFIQIRISKGGLIKTKRKRKQKRVKIAYEEIFVKNM 277

RESULT 12
AAR67994
ID AAR67994 standard; protein; 304 AA.
XX
AC AAR67994;
XX
DT 25-MAR-2003 (revised)
DT 13-AUG-1995 (first entry)
XX
DE Tissue factor pathway inhibitor.
XX
KW Yeast aspartic protease 3; YAP3; signal peptide; protein secretion;
KW tissue factor pathway inhibitor; TPPI.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..28
FT /label= sig_peptide
FT /note= "TPPI signal peptide"
XX
PN WO9502059-A1.
XX
PD 19-JAN-1995.
XX
PF 08-JUL-1994; 94WO-DK000281.
XX
PR 08-JUL-1993; 93DK-00000828.
XX
PA (NOVO ) NOVO-NORDISK AS.
XX
PI Christiansen L, Petersen JG;
XX
WPI; 1995-066903/09.
DR N-PSDB; AAQ81396.
XX
PT DNA construct encoding the yeast aspartic protease 3 signal peptide -
PT provides improved secretion of proteins in transformed yeast cells, such
PT as aprotinin and insulin.
XX
PS Disclosure; Page 27-28; 56pp; English.
XX
CC A SalI fragment encoding human tissue factor pathway inhibitor (TPPI) is
CC given in AAQ81396. It was used to construct expression vectors allowing
CC production of TPPI in Saccharomyces cerevisiae as fusions to the yeast
CC aspartic protease 3 (YAP3) signal peptide, facilitating secretion of the
CC recombinant TPPI. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 304 AA;
Query Match 100.0%; Score 1528; DB 2; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.4e-129;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DSEDEEHTITDTELPPLKLMHSFCAPKADGFCFKALMKRFFNIFTRQCEEFYGGCE 60
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Db 29 DSEDEEHTITDTELPPLKLMHSFCAPKADGFCFKALMKRFFNIFTRQCEEFYGGCE 88
QY 61 GNQRFESLECKKQCTRDNANRIIKTTLQOEKDPDFCFLEEDPGICRGYITRYFYNNQTK 120
Db 89 GNQRFESLECKKQCTRDNANRIIKTTLQOEKDPDFCFLEEDPGICRGYITRYFYNNQTK 148
QY 121 QCERFKYGGCLGNMNFETLECKNICEDGPNQFQVDNYGTQLNAVNNSLTPQSTKVPSSL 180
Db 149 QCERFKYGGCLGNMNFETLECKNICEDGPNQFQVDNYGTQLNAVNNSLTPQSTKVPSSL 208
QY 181 FEFHGPSWCLTPADRGGLCRANENRFFYNSVIGKCRPFKYSGCGGNENFTSKQECIRACK 240
Db 209 FEFHGPSWCLTPADRGGLCRANENRFFYNSVIGKCRPFKYSGCGGNENFTSKQECIRACK 268
QY 241 KGFIQIRISKGGLIKTKRKRKQKRVKIAYEEIFVKNM 276
Db 269 KGFIQIRISKGGLIKTKRKRKQKRVKIAYEEIFVKNM 304

RESULT 13
AAR81884
ID AAR81884 standard; protein; 304 AA.
XX
AC AAR81884;
XX
DT 18-MAR-1996 (first entry)
XX
DE Lipoprotein-associated coagulation inhibitor (LACI).
XX
KW Lipoprotein-associated coagulation inhibitor; LACI; kallikrein;
KW inhibitor; KIP; Kunitz domain; hereditary angioedema.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..28
FT /label= sig_peptide
FT Domain 50..107
FT /note= "Kunitz domain LACI-K1"
FT Domain 121..178
FT /note= "Kunitz domain LACI-K2"
FT Domain 213..270
FT /note= "Kunitz domain LACI-K3"
XX
PN WO9521601-A2.
XX
PD 17-AUG-1995.
XX
PF 11-JAN-1995; 95WO-US000299.
XX
PR 11-JAN-1994; 94US-00179964.
PR 10-MAR-1994; 94US-00208264.
XX
PA (PROT-) PROTEIN ENG CORP.
XX
PI Markland W, Ladner RC;
XX
WPI; 1995-292934/38.
XX
PT Kallikrein inhibiting proteins comprising a Kunitz domain homologous to
PT bovine pancreatic trypsin inhibitor - useful for preventing or treating
PT disorders attributable to excessive kallikrein activity, eg. in
PT hereditary angioedema.
XX
PS Disclosure; Page 24; 46pp; English.
XX
CC AAR81884 is the human lipoprotein-associated coagulation inhibitor LACI.
CC The Kunitz domain, LACI-K1, of LACI is a kallikrein inhibiting protein
CC (KIP) upon which the claimed KIPs of the invention are based. The KIPs
CC can be used for treating or preventing disorders attributable to
CC excessive kallikrein activity, e.g. hereditary angioedema. The KIPs can
CC also be used for assaying, purifying and in vivo imaging of kallikrein
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XX SQ Sequence 304 AA;
Query Match 100.0%; Score 1528; DB 2; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.4e-129;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DSEDEEHTIITDELPLPLKLMHSCAFKADGPKCAIMKRRFFNIFTRQCEEFYGGCE 60
DB 29 DSEDEEHTIITDELPLPLKLMHSCAFKADGPKCAIMKRRFFNIFTRQCEEFYGGCE 88
QY 61 GNQNFESLECKKMCCTRDNANRIIKTTLOQEKDPFCFLEEDPGICRGVITRYFYNNQTK 120
DB 89 GNQNFESLECKKMCCTRDNANRIIKTTLOQEKDPFCFLEEDPGICRGVITRYFYNNQTK 148
QY 121 QCERFKYGGCLGNMNFETLECKNICEDGPNQFVDNYGTQLNANVNSLTQSTKVPSL 180
DB 149 QCERFKYGGCLGNMNFETLECKNICEDGPNQFVDNYGTQLNANVNSLTQSTKVPSL 208
QY 181 FEHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFKYSGCGNENFTSKQECIRACK 240
DB 209 FEHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFKYSGCGNENFTSKQECIRACK 268
QY 241 KGFIQIRISKGGLIKTKRKRKQKVIAEIEIFVKM 276
DB 269 KGFIQIRISKGGLIKTKRKRKQKVIAEIEIFVKM 304

RESULT 14
AAAY49557
ID AAY49557 standard; protein; 304 AA.
XX AC AAY49557;
XX DT 13-JAN-2000 (first entry)
XX DE Human lipoprotein associated coagulation inhibitor protein sequence.
XX KW Human; coding sequence polymorphism; vascular pathology gene;
XX KW polymorphic site; phenotype correlation; forensic; paternity testing;
XX KW medicine; genetic analysis; vascular disease.
XX OS Homo sapiens.
XX PN WO9950454-A2.
XX PD 07-OCT-1999.
XX PF 26-MAR-1999; 99WO-US006473.
XX PR 01-APR-1998; 98US-00054272.
XX PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX PI Lander ES, Daley GQ, Cargill M, Ireland JS, Rozen SG;
XX WPI; 1999-620066/53.
XX DR N-PSDB; AAZ32166.
XX PT Determination of polymorphisms in genes, especially those identifying
XX PT predisposition to vascular disease.
XX PS Disclosure; Fig 10; 134pp; English.
XX CC AAZ32159 to AAZ32194 represent reference alleles for specifically claimed
XX CC nucleic acid sequences from the present invention which comprise
XX CC polymorphic sites as given in a table in the specification, selected from
XX CC 92 single nucleotide polymorphisms in which the nucleotide at the
XX CC polymorphic site is different from a nucleotide at the same site in a
XX CC reference allele. The nucleic acids, and primers and probes, are used to
XX CC identify polymorphisms, which may predispose an individual to disease,
XX CC especially a vascular disease. They can also be used in phenotype
XX CC correlations, forensics, paternity testing, medicine or genetic analysis.
```

```
CC AAY49550 to AAY49573 represent the proteins which correspond to some of
CC the reference alleles
XX SQ Sequence 304 AA;
Query Match 100.0%; Score 1528; DB 2; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.4e-129;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DSEDEEHTIITDELPLPLKLMHSCAFKADGPKCAIMKRRFFNIFTRQCEEFYGGCE 60
DB 29 DSEDEEHTIITDELPLPLKLMHSCAFKADGPKCAIMKRRFFNIFTRQCEEFYGGCE 88
QY 61 GNQNFESLECKKMCCTRDNANRIIKTTLOQEKDPFCFLEEDPGICRGVITRYFYNNQTK 120
DB 89 GNQNFESLECKKMCCTRDNANRIIKTTLOQEKDPFCFLEEDPGICRGVITRYFYNNQTK 148
QY 121 QCERFKYGGCLGNMNFETLECKNICEDGPNQFVDNYGTQLNANVNSLTQSTKVPSL 180
DB 149 QCERFKYGGCLGNMNFETLECKNICEDGPNQFVDNYGTQLNANVNSLTQSTKVPSL 208
QY 181 FEHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFKYSGCGNENFTSKQECIRACK 240
DB 209 FEHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFKYSGCGNENFTSKQECIRACK 268
QY 241 KGFIQIRISKGGLIKTKRKRKQKVIAEIEIFVKM 276
DB 269 KGFIQIRISKGGLIKTKRKRKQKVIAEIEIFVKM 304

RESULT 15
ADF09568
ID ADF09568 standard; protein; 304 AA.
XX AC ADF09568;
XX DT 12-FEB-2004 (first entry)
XX DE Human tissue factor pathway inhibitor SEQ ID NO:69.
XX KW human; protein-protein interaction; virucide; cytostatic; vaccine;
XX KW human papilloma virus; HPV; cancer.
XX OS Homo sapiens.
XX PN WO2003068940-A2.
XX PD 21-AUG-2003.
XX PF 14-FEB-2003; 2003WO-US004594.
XX PR 14-FEB-2002; 2002US-0356911P.
XX PA (CURA-) CURAGEN CORP.
XX PA (HOFF ) HOFFMANN LA ROCHE INC.
XX PI Jackson A, Ooi CE, Lewin DA, Cuthill S;
XX WPI; 2003-689668/65.
XX DR N-PSDB; ADF09675.
XX PT New purified complex comprising a first polypeptide and a second
XX PT polypeptide, useful for identifying agents for treating/preventing a
XX PT condition involving altered level of the complex e.g. human papilloma
XX PT virus infection, or cancer.
XX PS Example 3; SEQ ID NO 69; 156pp; English.
XX CC The invention relates to a novel purified complex comprising a first
XX CC polypeptide and a second polypeptide, where the polypeptides comprise
XX CC defined amino acid sequences listed in the specification, and where the
XX CC first polypeptide binds to the second polypeptide. A complex of the
XX CC invention has virucide and cytostatic activity, and may have a use as a
```

CC vaccine. The complex is useful for identifying agents for treating or
CC preventing a conditions involving altered level of the complex, e.g.
CC human papilloma virus (HPV) infection, or cancer. The compositions,
CC antibodies, vectors and methods are useful for treating such diseases.
CC The sequences shown in ADF09500-ADF09583 represent proteins of the
CC invention.

XX

SQ Sequence 304 AA;

Query Match 100.0%; Score 1528; DB 7; Length 304;
Best Local Similarity 100.0%; Pred. NO. 1.4e-129;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	DSEEDDEHTIIITDTELPPLKLMHSFCAPKADGCPCKAIWKRFNFNITRQCEFIYGGCE	60
Db	29	DSEEDDEHTIIITDTELPPLKLMHSFCAPKADGCPCKAIWKRFNFNITRQCEFIYGGCE	88
QY	61	GNQNPESLECKCKMCTRONANRIIKTTLQEKPDPCFLEEDPGICRGYITRYFYNNQTK	120
Db	89	GNQNPESLECKCKMCTRONANRIIKTTLQEKPDPCFLEEDPGICRGYITRYFYNNQTK	148
QY	121	QCERFKYGGCLGNMNFETLECKNICEDGPNQFOVDNYGTOLNANNSLTPQSTKVPSL	180
Db	149	QCERFKYGGCLGNMNFETLECKNICEDGPNQFOVDNYGTOLNANNSLTPQSTKVPSL	208
QY	181	FEFHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFKYSGCCGNENNFTSKQECCLACK	240
Db	209	FEFHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFKYSGCCGNENNFTSKQECCLACK	268
QY	241	KGFIOIRISKGGLIKTKRKKKORVKIAYEEIFVKM	276
Db	269	KGFIOIRISKGGLIKTKRKKKORVKIAYEEIFVKM	304

Search completed: April 16, 2005, 03:26:51
Job time : 176 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2005, 03:21:23 ; Search time 43 Seconds
(without alignments)
479.143 Million cell updates/sec

Title: US-10-753-079-1

Perfect score: 1528

Sequence: 1 DSEDEHHTITDTELPK.....RRKKQRVKIAYEIFVKQM 276

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_6/ptodata/1/iaa/5B.COMB.pap:*
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- 5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pap:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1528	100.0	276	2	US-08-796-850-1
2	1528	100.0	276	4	US-09-766-778-1
3	1528	100.0	277	1	US-07-844-297-1
4	1528	100.0	304	1	US-08-026-145-2
5	1528	100.0	304	1	US-08-446-646-9
6	1528	100.0	304	1	US-08-676-125A-18
7	1528	100.0	304	2	US-09-136-012A-18
8	1528	100.0	304	3	US-08-676-124-1
9	1528	100.0	304	3	US-08-208-264A-25
10	1528	100.0	304	3	US-09-414-878-1
11	1528	100.0	304	3	US-09-240-136-1
12	1528	100.0	304	3	US-09-421-097-25
13	1528	100.0	304	4	US-09-638-770A-1
14	1528	100.0	304	4	US-09-054-272-16
15	1528	100.0	304	6	5466783-2
16	1528	100.0	304	6	5466783-2
17	1528	100.0	352	3	US-08-854-764-2
18	1528	100.0	352	5	PCT-US95-09377-2
19	1528	100.0	381	4	US-09-949-016-7400
20	1525	99.8	276	1	US-08-437-841-9
21	1525	99.8	276	1	US-08-286-521-9
22	1525	99.8	276	1	US-08-436-175-9
23	1525	99.8	276	3	US-08-854-764-3
24	1525	99.8	276	3	US-08-943-682-9
25	1525	99.8	276	4	US-09-741-106-9
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29. 1522 99.6 304 4 US-08-627-676-2 Sequence 2, Appli
30. 1522 99.6 304 4 US-10-377-817-2 Sequence 2, Appli
31. 1521 99.3 276 1 US-07-828-920A-1 Sequence 1, Appli
32. 1517 99.3 304 4 US-09-763-565-2 Sequence 2, Appli
33. 1507 98.6 304 4 US-09-763-565-4 Sequence 4, Appli
34. 1447.5 94.7 291 4 US-10-000-489-48 Sequence 48, Appli
35. 1444.5 94.5 291 4 US-10-000-489-52 Sequence 52, Appli
36. 1180.5 77.3 213 6 5466783-25 Patent No. 5466783
37. 1180.5 77.3 213 6 5466783-25 Patent No. 5466783
38. 900 58.9 189 1 US-07-828-920A-7 Sequence 7, Appli
39. 897 58.7 161 1 US-08-437-841-19 Sequence 19, Appli
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42. 897 58.7 161 3 US-08-943-682-19 Sequence 19, Appli
43. 897 58.7 161 4 US-09-741-106-19 Sequence 19, Appli
44. 897 58.7 161 5 PCT-US95-09464-19 Sequence 19, Appli
45. 834 54.6 183 1 US-07-828-920A-5 Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-08-796-850-1
; Sequence 1, Application US/08796850
; Patent No. 5981471
; GENERAL INFORMATION:
; APPLICANT: Papathanassiou, Adonia E
; APPLICANT: Green, Shawn J.
; TITLE OF INVENTION: Compositions and Methods for Inhibiting
; TITLE OF INVENTION: Cellular Proliferation
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: U.S.A.
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/796,850
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Greene, Jamie L.
; REGISTRATION NUMBER: 32,467
; REFERENCE/DOCKET NUMBER: 05213-0290
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 818-3700
; TELEFAX: (404) 818-3799
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 276 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Active-site
; LOCATION: 2..3
; OTHER INFORMATION: /note= "Site of partial phosphorylation"

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FEATURE:
NAME/KEY: Active-site
LOCATION: 117..118
OTHER INFORMATION: /note= "Potential site for N-linked glycosylation"
FEATURE:
NAME/KEY: Active-site
LOCATION: 167..168
OTHER INFORMATION: /note= "Potential site for N-linked glycosylation"
FEATURE:
NAME/KEY: Active-site
LOCATION: 228..229
OTHER INFORMATION: /note= "Potential site for N-linked glycosylation"
FEATURE:
NAME/KEY: Domain
LOCATION: 26..76
OTHER INFORMATION: /label= Kunitz-1
FEATURE:
NAME/KEY: Domain
LOCATION: 97..147
OTHER INFORMATION: /label= Kunitz-2
FEATURE:
NAME/KEY: Domain
LOCATION: 189..239
OTHER INFORMATION: /label= Kunitz-3
SEQUENCE DESCRIPTION: SEQ ID NO: 1;
US-09-766-778-1

Query Match 100.0%; Score 1528; DB 2; Length 276;
Best Local Similarity 100.0%; Pred. No. 1.1e-145;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSEDEEHTIITDTELPPLKMHSCAFKADGPKCKAIKMRFFNFTQCEEFYGGCE 60
Db 1 DSEDEEHTIITDTELPPLKMHSCAFKADGPKCKAIKMRFFNFTQCEEFYGGCE 60

Qy 61 GQNRFESLECKKMCCTRDNANRIKTTLOQKPDGFCFLEEDPGICRGYITRYFNNQTK 120
Db 61 GQNRFESLECKKMCCTRDNANRIKTTLOQKPDGFCFLEEDPGICRGYITRYFNNQTK 120

Qy 121 QCEPKYGGCLGNMNFTELECKNICDGNPGFQVDNYGTLNANVNSLTPQSKVPSL 180
Db 121 QCEPKYGGCLGNMNFTELECKNICDGNPGFQVDNYGTLNANVNSLTPQSKVPSL 180

Qy 181 FEFGHPSWCLTPADRGLCRANENRYNSVIGKCPFKYSGCGNENFTSQECLACK 240
Db 181 FEFGHPSWCLTPADRGLCRANENRYNSVIGKCPFKYSGCGNENFTSQECLACK 240

Qy 241 KGFQIRISKGLIKTKRKQRKQKVIAVEEIPVKNM 276
Db 241 KGFQIRISKGLIKTKRKQRKQKVIAVEEIPVKNM 276

RESULT 2
US-09-766-778-1
Sequence 1, Application US/09766778
Patent No. 6734163
GENERAL INFORMATION:
APPLICANT: Papathanassiou, Adonia E
ADDRESSER: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.A.
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,778
FILING DATE: 22-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/227,955
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Greene, Jamie L.
REGISTRATION NUMBER: 32,467
REFERENCE/DOCKET NUMBER: 05213-0290
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 818-3700
TELEFAX: (404) 818-3799
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: Active-site
LOCATION: 2..3
OTHER INFORMATION: /note= "Site of partial phosphorylation"
FEATURE:
NAME/KEY: Active-site
LOCATION: 117..118
OTHER INFORMATION: /note= "Potential site for N-linked glycosylation"
FEATURE:
NAME/KEY: Active-site
LOCATION: 167..168
OTHER INFORMATION: /note= "Potential site for N-linked glycosylation"
FEATURE:
NAME/KEY: Active-site
LOCATION: 228..229
OTHER INFORMATION: /note= "Potential site for N-linked glycosylation"
FEATURE:
NAME/KEY: Domain
LOCATION: 26..76
OTHER INFORMATION: /label= Kunitz-1
FEATURE:
NAME/KEY: Domain
LOCATION: 97..147
OTHER INFORMATION: /label= Kunitz-2
FEATURE:
NAME/KEY: Domain
LOCATION: 189..239
OTHER INFORMATION: /label= Kunitz-3
SEQUENCE DESCRIPTION: SEQ ID NO: 1;
US-09-766-778-1

Query Match 100.0%; Score 1528; DB 2; Length 276;
Best Local Similarity 100.0%; Pred. No. 1.1e-145;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSEDEEHTIITDTELPPLKMHSCAFKADGPKCKAIKMRFFNFTQCEEFYGGCE 60
Db 1 DSEDEEHTIITDTELPPLKMHSCAFKADGPKCKAIKMRFFNFTQCEEFYGGCE 60

Qy 61 GQNRFESLECKKMCCTRDNANRIKTTLOQKPDGFCFLEEDPGICRGYITRYFNNQTK 120
Db 61 GQNRFESLECKKMCCTRDNANRIKTTLOQKPDGFCFLEEDPGICRGYITRYFNNQTK 120

Qy 121 QCEPKYGGCLGNMNFTELECKNICDGNPGFQVDNYGTLNANVNSLTPQSKVPSL 180
Db 121 QCEPKYGGCLGNMNFTELECKNICDGNPGFQVDNYGTLNANVNSLTPQSKVPSL 180

Qy 181 FEFGHPSWCLTPADRGLCRANENRYNSVIGKCPFKYSGCGNENFTSQECLACK 240
Db 181 FEFGHPSWCLTPADRGLCRANENRYNSVIGKCPFKYSGCGNENFTSQECLACK 240

Qy 241 KGFQIRISKGLIKTKRKQRKQKVIAVEEIPVKNM 276
Db 241 KGFQIRISKGLIKTKRKQRKQKVIAVEEIPVKNM 276

NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.A.
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Db 61 GQNRFSLECKKCKCTDNRNRIKTTLOQKDPFCLEEDPGICRGYITRYFYNNOTK 120
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Db 121 QCRFKYGGCLGNMNFETLECKNICEDGPNFGVDNYGTQLNANVNSLTQSTKVPSL 180
Qy 181 FEPHPSWCLTPADRGCLCRANENRYNSVIGKCRPFKYSGCGNENFTSKOECLACK 240
Db 181 FEPHPSWCLTPADRGCLCRANENRYNSVIGKCRPFKYSGCGNENFTSKOECLACK 240
Qy 241 KGFIORISKGLIKTKRKRKQKVIAEIEIFVKNM 276
Db 241 KGFIORISKGLIKTKRKRKQKVIAEIEIFVKNM 276

RESULT 3

US-07-844-297-1
; Sequence 1, Application US/07844297
; Patent No. 5212091
; GENERAL INFORMATION:
; APPLICANT: Diaz-Collier, Judy A.
; APPLICANT: Gustafson, Mark E.
; APPLICANT: Wun, Tze-Chen
; TITLE OF INVENTION: Method of Producing Tissue Factor
; TITLE OF INVENTION: Pathway Inhibitor
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A39G
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/844,297
; FILING DATE: 19920302
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: 07-21(819)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-844-297-1

Query Match 100.0%; Score 1528; DB 1; Length 277;
Best Local Similarity 100.0%; Pred. No. 1.1e-145;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 62 GQNRFSLECKKCKCTDNRNRIKTTLOQKDPFCLEEDPGICRGYITRYFYNNOTK 121
Qy 121 QCRFKYGGCLGNMNFETLECKNICEDGPNFGVDNYGTQLNANVNSLTQSTKVPSL 180
Db 122 QCRFKYGGCLGNMNFETLECKNICEDGPNFGVDNYGTQLNANVNSLTQSTKVPSL 181

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Db 182 FEPHPSWCLTPADRGCLCRANENRYNSVIGKCRPFKYSGCGNENFTSKOECLACK 241
Qy 241 KGFIORISKGLIKTKRKRKQKVIAEIEIFVKNM 276
Db 242 KGFIORISKGLIKTKRKRKQKVIAEIEIFVKNM 277

RESULT 4

US-08-026-145-2
; Sequence 2, Application US/08026145
; Patent No. 5378614
; GENERAL INFORMATION:
; APPLICANT: Petersen, Jens G. Liteke
; APPLICANT: No. 5378614dfang, Ole Juul
; TITLE OF INVENTION: Method for Making TFPI Analogues
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5378614o No. 5378614disk of No. 5378614th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6200
; CITY: New York
; STATE: N. Y.
; COUNTRY: United States of America
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/026,145
; FILING DATE: 19930302
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/828,920
; FILING DATE: 27-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DK/90/00212
; FILING DATE: 17-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 4080/89
; FILING DATE: 18-AUG-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Agtis, Cheryl H.
; REGISTRATION NUMBER: 34086
; REFERENCE/DOCKET NUMBER: 3321.214-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 304 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-026-145-2

Query Match 100.0%; Score 1528; DB 1; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.2e-145;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 29 DSEDEEHTIITDTELPLKLMHSCAFKADGPKCAIMKRPFFNIFTRQCEFIYGGCE 88
Qy 61 GQNRFSLECKKCKCTDNRNRIKTTLOQKDPFCLEEDPGICRGYITRYFYNNOTK 120
Db 89 GQNRFSLECKKCKCTDNRNRIKTTLOQKDPFCLEEDPGICRGYITRYFYNNOTK 148
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Db 149 QCRFKYGGCLGNMNFETLECKNICEDGPNFGVDNYGTQLNANVNSLTQSTKVPSL 208

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 Db 209 FEFHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFKYSGCGGNENFTSKQECRLACK 268
 QY 241 KGFIORISKGGLIKTKRKRKQKVIAEIEFVKM 276
 Db 269 KGFIORISKGGLIKTKRKRKQKVIAEIEFVKM 304

RESULT 5
 US-08-446-646-9
 ; Sequence 9, Application US/08446646
 ; Patent No. 5726038
 ; GENERAL INFORMATION:
 ; APPLICANT: Christiansen, Lars
 ; APPLICANT: Petersen, Jens G.
 ; TITLE OF INVENTION: A DNA Construct Encoding the YAP3 Signal
 ; TITLE OF INVENTION: Peptide
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: No. 57260380 No. 5726038disk of No. 5726038th America, Inc.
 ; STREET: 405 Lexington Avenue, 64th Floor
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: United States of America
 ; ZIP: 10174-6401
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/446,646
 ; FILING DATE: 25-MAY-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lambiris, Elias J.
 ; REGISTRATION NUMBER: 33,728
 ; REFERENCE/DOCKET NUMBER: 3987.204-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-867-0123
 ; TELEFAX: 212-878-9655
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 304 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-446-646-9

Query Match 100.0%; Score 1528; DB 1; Length 304;
 Best Local Similarity 100.0%; Pred. No. 1.2e-145;
 Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DSEDEEHTIITDTELPPLKLMHSFCAPKADGPKAIMKRFNFITRQCEEFYIGGCE 60
 Db 29 DSEDEEHTIITDTELPPLKLMHSFCAPKADGPKAIMKRFNFITRQCEEFYIGGCE 88
 QY 61 GNQNFESLECKKWCRTDNANRIKTTLOQEKPDFCFLEEDPGICRGYITRYFYNNQTK 120
 Db 89 GNQNFESLECKKWCRTDNANRIKTTLOQEKPDFCFLEEDPGICRGYITRYFYNNQTK 148
 QY 121 QCERFKYGGCLGNMNNFETLECKNICEDGPNQFQVNDYGTQLNAVNNSLTPQSTKVPSL 180
 Db 149 QCERFKYGGCLGNMNNFETLECKNICEDGPNQFQVNDYGTQLNAVNNSLTPQSTKVPSL 208
 QY 181 FEFHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFKYSGCGGNENFTSKQECRLACK 240
 Db 209 FEFHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFKYSGCGGNENFTSKQECRLACK 268
 QY 241 KGFIORISKGGLIKTKRKRKQKVIAEIEFVKM 276

Db 269 KGFIORISKGGLIKTKRKRKQKVIAEIEFVKM 304

RESULT 6
 US-08-676-125A-18
 ; Sequence 18, Application US/08676125A
 ; Patent No. 5795865
 ; GENERAL INFORMATION:
 ; APPLICANT: MARKLAND, William
 ; APPLICANT: LADNER, Robert Charles
 ; TITLE OF INVENTION: KALLIKREIN-INHIBITING "KUNITZ DOMAIN" PROTEINS AND ANALOGUES
 ; NUMBER OF SEQUENCES: 70
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Yankwich & Associates
 ; STREET: 130 Bishop Allen Drive, fifth floor
 ; CITY: Cambridge
 ; STATE: Massachusetts
 ; COUNTRY: United States of America
 ; ZIP: 02139
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Word for Windows 6.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/676,125A
 ; FILING DATE: 25 September 1996
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/00299
 ; FILING DATE: 11 January 1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/179,964
 ; FILING DATE: 11 January 1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/208,264
 ; FILING DATE: 10 March 1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: YANKWICH, Leon R.
 ; REGISTRATION NUMBER: 30,237
 ; REFERENCE/DOCKET NUMBER: DYX-006.2P US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 491-4343
 ; TELEFAX: (617) 491-8801
 ; INFORMATION FOR SEQ ID NO: 18:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 304 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-676-125A-18

Query Match 100.0%; Score 1528; DB 1; Length 304;
 Best Local Similarity 100.0%; Pred. No. 1.2e-145;
 Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DSEDEEHTIITDTELPPLKLMHSFCAPKADGPKAIMKRFNFITRQCEEFYIGGCE 60
 Db 29 DSEDEEHTIITDTELPPLKLMHSFCAPKADGPKAIMKRFNFITRQCEEFYIGGCE 88
 QY 61 GNQNFESLECKKWCRTDNANRIKTTLOQEKPDFCFLEEDPGICRGYITRYFYNNQTK 120
 Db 89 GNQNFESLECKKWCRTDNANRIKTTLOQEKPDFCFLEEDPGICRGYITRYFYNNQTK 148
 QY 121 QCERFKYGGCLGNMNNFETLECKNICEDGPNQFQVNDYGTQLNAVNNSLTPQSTKVPSL 180
 Db 149 QCERFKYGGCLGNMNNFETLECKNICEDGPNQFQVNDYGTQLNAVNNSLTPQSTKVPSL 208
 QY 181 FEFHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFKYSGCGGNENFTSKQECRLACK 240
 Db 209 FEFHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFKYSGCGGNENFTSKQECRLACK 268

QY 241 KGFIQRISKGLIKTKRKRKQKVIAVEEIVFKNM 276
DB 269 KGFIQRISKGLIKTKRKRKQKVIAVEEIVFKNM 304

RESULT 7

US-09-136-012A-18
; Sequence 18, Application US/09136012A
; Patent No. 5994125
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP
; APPLICANT: MARKLAND, William
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: KALLIKREIN-INHIBITING "KUNITZ DOMAIN" PROTEINS
; TITLE OF INVENTION: AND ANALOGUES THEREOF
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive, fifth floor
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5-inch diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: Microsoft Word 97 SR-1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09136,012A
; FILING DATE: 17-August-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/676,125
; FILING DATE: 25-September-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00299
; FILING DATE: 11-January-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/208,264
; FILING DATE: 10-March-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/179,964
; FILING DATE: 11-January-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: YANKWICH, Leon R.
; REGISTRATION NUMBER: 30,237
; NAME: ZWICKER, Kenneth P.
; REGISTRATION NUMBER: 43,310
; REFERENCE/DOCKET NUMBER: DYX-006.2P US-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 491-4343
; TELEFAX: (617) 491-8801
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 304 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-136-012A-18

Query Match 100.0%; Score 1528; DB 2; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.2e-145;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEEHTIITDELPLPKLMHSCAFKADGPKCAIMKRRFFNIFTRQCEEFYGGCE 60
DB 29 DSEDEEHTIITDELPLPKLMHSCAFKADGPKCAIMKRRFFNIFTRQCEEFYGGCE 88
QY 61 GQNRPFESLECKKMCCTRDNANRIKTTIQEKPDPFCFLEEDPGICRGVITRYFYNNQTK 120
DB 89 GQNRPFESLECKKMCCTRDNANRIKTTIQEKPDPFCFLEEDPGICRGVITRYFYNNQTK 148

QY 121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNQFQVDNYGTQLNAVNSLTPOSTKVPSSL 180
DB 149 QCERFKYGGCLGNMNNFETLEECKNICEDGPNQFQVDNYGTQLNAVNSLTPOSTKVPSSL 208
QY 181 FEFHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFKYSGCGGNENNFTSKQECLRACK 240
DB 209 FEFHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFKYSGCGGNENNFTSKQECLRACK 268
QY 241 KGFIQRISKGLIKTKRKRKQKVIAVEEIVFKNM 276
DB 269 KGFIQRISKGLIKTKRKRKQKVIAVEEIVFKNM 304

RESULT 8

US-08-676-124-1
; Sequence 1, Application US/08676124
; Patent No. 6010880
; GENERAL INFORMATION:
; APPLICANT: MARKLAND, William
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: INHIBITORS OF HUMAN PLASMIN DERIVED
; TITLE OF INVENTION: FROM FROM THE KUNITZ DOMAINS
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/676,124
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00298
; FILING DATE: 11-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/179,658
; FILING DATE: 11-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/208,265
; FILING DATE: 10-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, IVER P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: MARKLAND-3B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 304 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-676-124-1

Query Match 100.0%; Score 1528; DB 3; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.2e-145;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEEHTIITDELPLPKLMHSCAFKADGPKCAIMKRRFFNIFTRQCEEFYGGCE 60
DB 29 DSEDEEHTIITDELPLPKLMHSCAFKADGPKCAIMKRRFFNIFTRQCEEFYGGCE 88
QY 61 GQNRPFESLECKKMCCTRDNANRIKTTIQEKPDPFCFLEEDPGICRGVITRYFYNNQTK 120

Db 89 QNQNRFESLECKKMCCTRDNANRIKTLQOEKDPDFCFLEEDPGICRGYITRYFNNQTK 148
Qy 121 QCEPKYGGCLGNMNNFETLECKNICEDGPNQFQVDNYGTOLNANNVNSLTPOSTKVPSL 180
Db 149 QCEPKYGGCLGNMNNFETLECKNICEDGPNQFQVDNYGTOLNANNVNSLTPOSTKVPSL 208
Qy 181 FEFHGPSWCLTPADRGCLCRANENRFFYNSVIGKCRPFKYSGCGNENFTSKQECCLACK 240
Db 209 FEFHGPSWCLTPADRGCLCRANENRFFYNSVIGKCRPFKYSGCGNENFTSKQECCLACK 268
Qy 241 KGFQIRISKGLIKTKRKRKKORVKIAYEEIFVKNM 276
Db 269 KGFQIRISKGLIKTKRKRKKORVKIAYEEIFVKNM 304

RESULT 9

US-08-208-264A-25
; Sequence 25, Application US/08208264A
; Patent No. 6057287
; GENERAL INFORMATION:
; APPLICANT: MARKLAND, William
; APPLICANT: LADNER, Robert C
; TITLE OF INVENTION: KALLIKREIN-BINDING "KUNITZ DOMAIN"
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5-inch diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 95
; SOFTWARE: Microsoft Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/208,264A
; FILING DATE: 10-MAR-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/179,964
; FILING DATE: 11-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Leon R. Yankwich
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: DYX-006.1 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-491-4343
; TELEFAX: 617-491-8801
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 304 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-208-264A-25

Query Match 100.0%; Score 1528; DB 3; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.2e-145;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DSEDEEHTITDTEPLPLKMHSCAFKADGPKCKAIKMKFFNIFTRQCEEFYGGCE 60
Db 29 DSEDEEHTITDTEPLPLKMHSCAFKADGPKCKAIKMKFFNIFTRQCEEFYGGCE 88
Qy 61 QNQNRFESLECKKMCCTRDNANRIKTLQOEKDPDFCFLEEDPGICRGYITRYFNNQTK 120
Db 89 QNQNRFESLECKKMCCTRDNANRIKTLQOEKDPDFCFLEEDPGICRGYITRYFNNQTK 148

Qy 121 QCEPKYGGCLGNMNNFETLECKNICEDGPNQFQVDNYGTOLNANNVNSLTPOSTKVPSL 180
Db 149 QCEPKYGGCLGNMNNFETLECKNICEDGPNQFQVDNYGTOLNANNVNSLTPOSTKVPSL 208
Qy 181 FEFHGPSWCLTPADRGCLCRANENRFFYNSVIGKCRPFKYSGCGNENFTSKQECCLACK 240
Db 209 FEFHGPSWCLTPADRGCLCRANENRFFYNSVIGKCRPFKYSGCGNENFTSKQECCLACK 268
Qy 241 KGFQIRISKGLIKTKRKRKKORVKIAYEEIFVKNM 276
Db 269 KGFQIRISKGLIKTKRKRKKORVKIAYEEIFVKNM 304

RESULT 10

US-09-414-878-1
; Sequence 1, Application US/09414878
; Patent No. 6071723
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP
; APPLICANT: MARKLAND, William
; APPLICANT: LADNER, Robert C
; TITLE OF INVENTION: Inhibitors of Human Plamin Derived
; FROM THE KUNITZ DOMAINS
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5-inch diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: Microsoft Word 97 SR-1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/414,878
; FILING DATE: (concurrently herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/240,136
; FILING DATE: 29-JAN-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/676,124
; FILING DATE: 07-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00298
; FILING DATE: 11-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/208,265
; FILING DATE: 10-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/179,685
; FILING DATE: 11-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: YANKWICH, Leon R
; REGISTRATION NUMBER: 30,237
; NAME: ZWICKER, Kenneth P
; REGISTRATION NUMBER: 43,310
; REFERENCE/DOCKET NUMBER: DYX-007.2P US-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-491-4343
; TELEFAX: 617-491-8801
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 304 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-414-878-1

Query Match 100.0%; Score 1528; DB 3; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.2e-145; Indels 0; Gaps 0;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DSEDEEHTIITDTELPPLKMHSCAFKADGPKCAIMKRPFFNIFTRQCEEFYGGCE 60
DB 29 DSEDEEHTIITDTELPPLKMHSCAFKADGPKCAIMKRPFFNIFTRQCEEFYGGCE 88
QY 61 GQNRPFESLECKKMCCTRDANRIIKTTLOQEKDPFCFLEEDPGICRGVITRYFYNNQTK 120
DB 89 GQNRPFESLECKKMCCTRDANRIIKTTLOQEKDPFCFLEEDPGICRGVITRYFYNNQTK 148
QY 121 QCEPFYGGCLGNMNFETLECKNICEDGPNQFQVDNYGTQLNNAVNSLTPQSTKVPSSL 180
DB 149 QCEPFYGGCLGNMNFETLECKNICEDGPNQFQVDNYGTQLNNAVNSLTPQSTKVPSSL 208
QY 181 FEFHGPSWCLTPADRGCLCRANENRYFNSVIGKCRPFYSGCGGNNFTSKQECIRACK 240
DB 209 FEFHGPSWCLTPADRGCLCRANENRYFNSVIGKCRPFYSGCGGNNFTSKQECIRACK 268
QY 241 KGFIQRIISGGLIKTKRKQRKQVIAVEEIFVKNM 276
DB 269 KGFIQRIISGGLIKTKRKQRKQVIAVEEIFVKNM 304

RESULT 11

US-09-240-136-1

; Sequence 1, Application US/09240136

; Patent No. 6103499

; GENERAL INFORMATION:

; APPLICANT: DYAX CORP

; APPLICANT: MARKLAND, William

; APPLICANT: LADNER, Robert C

; TITLE OF INVENTION: Inhibitors of Human Plamin Derived

; NUMBER OF SEQUENCES: 139

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Yankwich & Associates

; STREET: 130 Bishop Allen Drive

; CITY: Cambridge

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02139

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5-inch diskette

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Microsoft Windows 98

; SOFTWARE: Microsoft Word 97 SR-1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/240,136

; FILING DATE: (concurrently herewith)

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/676,124

; FILING DATE: 07-JAN-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/00298

; FILING DATE: 11-JAN-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/208,265

; FILING DATE: 10-MAR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/179,685

; FILING DATE: 11-JAN-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: YANKWICH, Leon R

; REGISTRATION NUMBER: 30,237

; NAME: ZWICKER, Kenneth P

; REGISTRATION NUMBER: 43,310

; REFERENCE/DOCKET NUMBER: DYX-007.2P US-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-491-4343

; TELEFAX: 617-491-8801

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 304 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-240-136-1

Query Match 100.0%; Score 1528; DB 3; Length 304;

Best Local Similarity 100.0%; Pred. No. 1.2e-145;

Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEEHTIITDTELPPLKMHSCAFKADGPKCAIMKRPFFNIFTRQCEEFYGGCE 60
DB 29 DSEDEEHTIITDTELPPLKMHSCAFKADGPKCAIMKRPFFNIFTRQCEEFYGGCE 88
QY 61 GQNRPFESLECKKMCCTRDANRIIKTTLOQEKDPFCFLEEDPGICRGVITRYFYNNQTK 120
DB 89 GQNRPFESLECKKMCCTRDANRIIKTTLOQEKDPFCFLEEDPGICRGVITRYFYNNQTK 148
QY 121 QCEPFYGGCLGNMNFETLECKNICEDGPNQFQVDNYGTQLNNAVNSLTPQSTKVPSSL 180
DB 149 QCEPFYGGCLGNMNFETLECKNICEDGPNQFQVDNYGTQLNNAVNSLTPQSTKVPSSL 208
QY 181 FEFHGPSWCLTPADRGCLCRANENRYFNSVIGKCRPFYSGCGGNNFTSKQECIRACK 240
DB 209 FEFHGPSWCLTPADRGCLCRANENRYFNSVIGKCRPFYSGCGGNNFTSKQECIRACK 268
QY 241 KGFIQRIISGGLIKTKRKQRKQVIAVEEIFVKNM 276
DB 269 KGFIQRIISGGLIKTKRKQRKQVIAVEEIFVKNM 304

RESULT 12

US-09-421-097-25

; Sequence 25, Application US/09421097

; Patent No. 633402

; GENERAL INFORMATION:

; APPLICANT: MARKLAND, William

; APPLICANT: LADNER, Robert C

; TITLE OF INVENTION: KALLIKREIN-BINDING "KUNITZ DOMAIN"

; TITLE OF INVENTION: PROTEINS AND ANALOGUES THEREOF

; NUMBER OF SEQUENCES: 61

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Yankwich & Associates

; STREET: 130 Bishop Allen Drive

; CITY: Cambridge

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02139

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5-inch diskette

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Microsoft Windows 98

; SOFTWARE: Microsoft Word 97

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/421,097

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/208,264

; FILING DATE: 10-MAR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/179,964

; FILING DATE: 11-JAN-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Leon R. Yankwich

; REGISTRATION NUMBER: 30,237

; REFERENCE/DOCKET NUMBER: DYX-006.1 US-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-491-4343

; TELEFAX: 617-491-8801

; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 304 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-421-097-25

Query Match 100.0%; Score 1528; DB 3; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.2e-145;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEHTIITDELPLPLKMHSCAFKADGPKCAIMKRRFFNIFTRQCEEFYGGCE 60
DB 29 DSEDEHTIITDELPLPLKMHSCAFKADGPKCAIMKRRFFNIFTRQCEEFYGGCE 88
QY 61 GQNRFESLECKKMTNRNANRIKTTLOQEKPDFCFLEEDPGICRGYITRYFNNQTK 120
DB 89 GQNRFESLECKKMTNRNANRIKTTLOQEKPDFCFLEEDPGICRGYITRYFNNQTK 148
QY 121 QCFERFYGGCLGNMNFETLEECNICEDGPNQFQVDNYGTOLNANVNSLTPOSTKVP 180
DB 149 QCFERFYGGCLGNMNFETLEECNICEDGPNQFQVDNYGTOLNANVNSLTPOSTKVP 208
QY 181 FEFHGPSWCLTPADRGGLCRANENRFYNSVIGKCRPFYSGCGGNENNFTSKQEC 240
DB 209 FEFHGPSWCLTPADRGGLCRANENRFYNSVIGKCRPFYSGCGGNENNFTSKQEC 268
QY 241 KGFIORISKGLIKTKRKKQKQVIAEIEFVKNM 276
DB 269 KGFIORISKGLIKTKRKKQKQVIAEIEFVKNM 304

RESULT 13

US-09-638-770A-1
; Sequence 1, Application US/09638770A
; Patent No. 6423499
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP
; MARKLAND, William
; LADNER, Robert C
; TITLE OF INVENTION: Inhibitors of Human Plasmin Derived
; FROM THE KUNITZ DOMAINS
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5-inch diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: Microsoft Word 97 SR-1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/638,770A
; FILING DATE: 15-Aug-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/676,124
; FILING DATE: 07-JAN-1997
; APPLICATION NUMBER: PCT/US95/00298
; FILING DATE: 11-JAN-1995
; APPLICATION NUMBER: 08/208,265
; FILING DATE: 10-MAR-1994
; APPLICATION NUMBER: 08/179,685
; FILING DATE: 11-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: ZWICKER, Kenneth P
; REGISTRATION NUMBER: 43,310

; REFERENCE/DOCKET NUMBER: DYX-007.2P US-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-491-4343
; TELEFAX: 617-491-8801

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 304 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-638-770A-1

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Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GQNRFESLECKKMTNRNANRIKTTLOQEKPDFCFLEEDPGICRGYITRYFNNQTK 120
DB 89 GQNRFESLECKKMTNRNANRIKTTLOQEKPDFCFLEEDPGICRGYITRYFNNQTK 148
QY 121 QCFERFYGGCLGNMNFETLEECNICEDGPNQFQVDNYGTOLNANVNSLTPOSTKVP 180
DB 149 QCFERFYGGCLGNMNFETLEECNICEDGPNQFQVDNYGTOLNANVNSLTPOSTKVP 208
QY 181 FEFHGPSWCLTPADRGGLCRANENRFYNSVIGKCRPFYSGCGGNENNFTSKQEC 240
DB 209 FEFHGPSWCLTPADRGGLCRANENRFYNSVIGKCRPFYSGCGGNENNFTSKQEC 268
QY 241 KGFIORISKGLIKTKRKKQKQVIAEIEFVKNM 276
DB 269 KGFIORISKGLIKTKRKKQKQVIAEIEFVKNM 304

RESULT 14

US-09-054-272-16
; Sequence 16, Application US/09054272
; Patent No. 6692909
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Daley, George O.
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Rozen, Steven G.
; TITLE OF INVENTION: CODING SEQUENCE POLYMORPHISMS
; IN VASCULAR PATHOLOGY GENES
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054,272
; FILING DATE: 01-APR-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia

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;
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WHI98-05
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 304 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
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US-09-054-272-16
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QY 61 GQNRFSLEECKKWCTRDNANRIIKTTIQEKPDPFCLEEDPGICRGYITRYFYNNQTK 120
DB 89 GQNRFSLEECKKWCTRDNANRIIKTTIQEKPDPFCLEEDPGICRGYITRYFYNNQTK 148
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DB 149 QCERFKYGGCLGNMNFLECKNICEDGPNGFQVDNYGTQLNAVNNSLTPQSTKVPSL 208
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DB 209 FEFHGPSWCLTPADRGCLCRANENRFFYNSVIGKCRPFKYSGCGGNENFTSKQECCLRACK 268
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RESULT 15
5466783-2
; Patent No. 5466783
; APPLICANT: Wun, Tze-Chien, Kretzmer, Kuniko K.; Broze,
; George J. Jr.
; TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
;
; NUMBER OF SEQUENCES: 26
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/93,285
; FILING DATE: 15-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 566,280
; FILING DATE: 13-AUG-1990
; APPLICATION NUMBER: 123,753
; FILING DATE: 23-NOV-1987
; APPLICATION NUMBER: 77,366
; FILING DATE: 23-JUL-1987
; SEQ ID NO: 2:
; LENGTH: 304
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DB 29 DSEDEEHTIITDTLPLPLKLMHSFCAPKADGPKCAIMKRFFNIFTRQCEEFYGGCE 88
QY 61 GQNRFSLEECKKWCTRDNANRIIKTTIQEKPDPFCLEEDPGICRGYITRYFYNNQTK 120
DB 89 GQNRFSLEECKKWCTRDNANRIIKTTIQEKPDPFCLEEDPGICRGYITRYFYNNQTK 148
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QY 121 QCERFKYGGCLGNMNFLECKNICEDGPNGFQVDNYGTQLNAVNNSLTPQSTKVPSL 180
DB 149 QCERFKYGGCLGNMNFLECKNICEDGPNGFQVDNYGTQLNAVNNSLTPQSTKVPSL 208
QY 181 FEFHGPSWCLTPADRGCLCRANENRFFYNSVIGKCRPFKYSGCGGNENFTSKQECCLRACK 240
DB 209 FEFHGPSWCLTPADRGCLCRANENRFFYNSVIGKCRPFKYSGCGGNENFTSKQECCLRACK 268
QY 241 KGFIQRIKGGGLIKTKRKRKQKVIAEIEIFVKNM 276
DB 269 KGFIQRIKGGGLIKTKRKRKQKVIAEIEIFVKNM 304
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Search completed: April 16, 2005, 03:29:35
Job time : 44 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 16, 2005, 03:16:28 ; Search time 60 Seconds
(without alignments)
2355.564 Million cell updates/sec

Title: US-10-753-079-1

Perfect score: 1528

Sequence: 1 DSEDEDEHTITDTELPPLK.....RKRKQKVAYEIEIFVKNM 276

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1528	100.0	304	1	TPPI_HUMAN
2	1447	94.7	304	1	TPPI_MACMU
3	1127	73.8	300	1	TPPI_RABIT
4	993	65.0	396	2	P19761_oryctolagus
5	934.5	61.2	302	1	Q28874 canis famil
6	886	58.0	306	1	Q2445 rattus norv
7	607	39.7	235	2	O54819 mus musculu
8	607	39.7	235	2	Q8BSB7 mus musculu
9	537.5	35.2	279	2	Q8C180 mus musculu
10	518	33.9	287	2	Q7Z342 brachydanio
11	463	30.3	224	2	O93424 cyprinus ca
12	446	29.2	277	2	Q7T025 xenopus lae
13	414.5	27.1	759	2	Q8AYE1 ancylostoma
14	392	25.7	234	2	Q8IT91 ancylostoma
15	388.5	25.4	2419	2	Q7YRQ8 bos taurus
16	384.5	25.2	235	1	Q7PXZ1 anopheles g
17	378.5	24.8	224	2	P48307 homo sapien
18	373	24.4	3198	2	Q8NAK6 Q8NAK6
19	360	23.6	2772	2	Q8U8G8 Q8U8G8
20	360	23.6	2776	2	Q8VAV4 Q8VAV4
21	360	23.6	2894	2	Q869A0 Q869A0
22	360	23.6	2898	2	Q8KX22 Q8KX22
23	358.5	23.5	1487	2	Q86829 Q86829
24	355.5	23.3	1558	2	Q8MPV5 Q8MPV5
25	355.5	23.3	1567	2	Q8I710 Q8I710
26	353	23.1	230	1	Q76840 Q76840
27	351.5	23.0	2174	2	Q35536 Q35536
28	350.5	22.9	2225	2	Q9GQR0 Q9GQR0
29	347	22.7	1474	2	Q45881 Q45881
30	341.5	22.3	327	2	O62504 O62504
31	341	22.3	230	2	Q6IND9 Q6IND9
32	341	22.3	1572	2	Q8NE89 Q8NE89
33	340	22.3	922	2	Q21418 Q21418
34	337	22.1	1297	2	Q9N343 Q9N343
35	334.5	21.9	988	2	Q22685 Q22685
36	332.5	21.8	1416	1	YN81_CABEL
37	327	21.4	1599	2	Q09983 Q09983
38	314.5	20.6	142	2	Q8WPI2 Q8WPI2
39	309	20.2	1949	2	Q8MXG3 Q8MXG3
40	303.5	19.9	142	2	Q8WPI3 Q8WPI3
41	303	19.8	1391	2	Q19021 Q19021
42	302.5	19.8	1743	2	Q9XW55 Q9XW55
43	296.5	19.4	1043	2	Q17644 Q17644
44	291	19.0	151	2	Q6T269 Q6T269
45	286.5	18.8	167	2	Q8NE89 Q8NE89

ALIGNMENTS

RESULT 1

ID	TFPI_HUMAN	STANDARD;	PRT;	304 AA.
AC	P10646; Q95103;			
DT	01-JUL-1989 (Rel. 11, Created)			
DT	01-JUL-1989 (Rel. 11, Last sequence update)			
DT	25-JAN-2005 (Rel. 46, Last annotation update)			
DE	Tissue factor pathway inhibitor precursor (TFPI) (Lipoprotein-			
DE	associated coagulation inhibitor) (LACI) (Extrinsic pathway inhibitor)			
DE	(EPI).			
GN	Name=TFPI; Synonyms=LACI, TFPI1;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).			
RX	MEDLINE=88198127; PubMed=2452157;			
RA	Wun T.-C., Kretzmer K.K., Girard T.J., Miletich J.P., Broze G.J. Jr.;			
RT	"Cloning and characterization of a cDNA coding for the lipoprotein-			
RT	associated coagulation inhibitor shows that it consists of three			
RT	tandem Kunitz-type inhibitory domains.";			
RL	J. Biol. Chem. 263:6001-6004(1988).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).			
RX	MEDLINE=91129227; PubMed=1993173;			
RA	van der Logt C.P.E., Reitsma P.H., Bertina R.M.;			
RT	"Intron-exon organization of the human gene coding for the			
RT	lipoprotein-associated coagulation inhibitor: the factor Xa dependent			
RT	inhibitor of the extrinsic pathway of coagulation.";			
RL	Biochemistry 30:1571-1577(1991).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).			
RX	MEDLINE=91161593; PubMed=2002045;			
RA	Girard T.J., Eddy R., Wesselschmidt R.L., Macphail L.A., Likert K.M.,			
RA	Byers M.G., Shows T.B., Broze G.J. Jr.;			
RT	"Structure of the human lipoprotein-associated coagulation inhibitor			
RT	gene. Intron/exon gene organization and localization of the gene to			
RL	chromosome 2.";			
RN	J. Biol. Chem. 266:5036-5041(1991).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).			
RX	MEDLINE=89388722; PubMed=2781520; DOI=10.1016/0049-3848(89)90454-4;			
RA	Girard T.J., Warren L.A., Novotny W.F., Bejcek B.E., Miletich J.P.,			
RA	Broze G.J. Jr.;			
RT	"Identification of the 1.4 kb and 4.0 kb messages for the lipoprotein			
RT	associated coagulation inhibitor and expression of the encoded			
RL	protein.";			
RL	Thromb. Res. 55:37-50(1989).			
RN	[5]			
RP	SEQUENCE FROM N.A. (ISOFORM BETA).			
RA	Chang J.-Y., Monroe D.M., Roberts H.R.;			
RL	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.			
RN	[6]			

O44938 haemochus
Q21418 caenorhabdi
Q9N343 caenorhabdi
Q22685 caenorhabdi
Q03610 caenorhabdi
Q09983 caenorhabdi
Q8WPI2 boophilus m
Q8MXG3 caenorhabdi
Q8WPI3 boophilus m
Q19021 caenorhabdi
Q9XW55 caenorhabdi
O17644 caenorhabdi
Q6T269 bitis gabon
Q8NE89 homo sapien

SEQUENCE FROM N.A. (ISOFORM ALPHA).
Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C.,
Ahearn M.O., Kuldaneck S.A., Rajkumar N., Toth E.J., Yi Q.,
Nickerson D.A.;
"SeattleSeqs.NHLBI HL66682 program for genomic applications, UW-
FHCRS, Seattle, WA (URL: <http://pga.gs.washington.edu/>);
Submitted (MAR-2003) to the ENBL/GenBank/DBJ databases.
[7]
SEQUENCE FROM N.A. (ISOFORM BETA).
TISSUE=Pancreas;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins B.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richardson S., Worley K.C., Hale S.E., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Helton E., Kettner M., Madan A.C., Rodriguez S., Sanchez A.,
Blakesley R.C., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[8]
SEQUENCE OF 29-50.
MEDLINE=90036996; PubMed=3553722;
Novotny W.F., Girard T.J., Miletich J.P., Broze G.J. Jr.;
"Purification and characterization of the lipoprotein-associated
coagulation inhibitor from human plasma.";
J. Biol. Chem. 264:18832-18837(1989).
[9]
SEQUENCE OF 29-43.
PubMed=15340161; DOI=10.1110/ps.04682504;
Zhang Z., Hensel W.J.;
"Signal peptide prediction based on analysis of experimentally
verified cleavage sites.";
Protein Sci. 13:2819-2824(2004).
[10]
INHIBITORY SITES.
MEDLINE=89181950; PubMed=2927510; DOI=10.1038/339518a0;
Girard T.J., Warren L.A., Novotny W.F., Likert K.M., Brown S.G.,
Miletich J.P., Broze G.J. Jr.;
"Functional significance of the Kunitz-type inhibitory domains of
lipoprotein-associated coagulation inhibitor.";
Nature 338:518-520(1989).
[11]
CARBOHYDRATE-LINKAGE SITES.
MEDLINE=96224851; PubMed=8639592; DOI=10.1021/bi9524880;
Nakahara Y., Miyata T., Hamuro T., Funatsu A., Miyagi M.,
Tsunasawa S., Kato H.;
"Amino acid sequence and carbohydrate structure of a recombinant human
tissue factor pathway inhibitor expressed in Chinese hamster ovary
cells: one N- and two O-linked carbohydrate chains are located between
Kunitz domains 2 and 3 and one N-linked carbohydrate chain is in
Kunitz domain 2.";
Biochemistry 35:6450-6459(1996).
[12]
REVIEW.
MEDLINE=91104709; PubMed=2271516;
Broze G.J. Jr., Girard T.J., Novotny W.F.;
"Regulation of coagulation by a multivalent Kunitz-type inhibitor.";
Biochemistry 29:7539-7546(1990).
[13]
X-RAY CRYSTALLOGRAPHY (2.6 ÅNGSTRÖMS) OF 121-178 IN COMPLEX WITH
TRYPSIN.

MEDLINE=97390427; PubMed=9242660; DOI=10.1074/jbc.272.32.19931;
Stubbs M.T., Morenweiser R., Stuerzbecher J., Bauer M., Bode W.,
Huber R., Piechotta G.P., Matschner G., Sommerhoff C.P., Fritz H.,
Auerwald E.A.;
RT "The three-dimensional structure of recombinant leech-derived trypsinase
inhibitor in complex with trypsin. Implications for the structure of
human mast cell trypsinase and its inhibition.";
J. Biol. Chem. 272:19931-19937(1997).
[14]
STRUCTURE BY NMR OF 121-182.
MEDLINE=97342711; PubMed=9199408; DOI=10.1006/jmbi.1997.1029;
Burgering M.J.M., Orbons L.P.M., van der Doelen A., Mulders J.,
Theunissen H.J.M., Grooteveld P.D.J., Bode W., Huber R., Stubbs M.T.;
RA "The second Kunitz domain of human tissue factor pathway inhibitor:
cloning, structure determination and interaction with factor Xa".
J. Mol. Biol. 269:395-407(1997).
[15]
STRUCTURE BY NMR OF 210-270.
PubMed=11772005; DOI=10.1021/bi011299g;
Mine S., Yamazaki T., Miyata T., Hara S., Kato H.;
RA "Structural mechanism for heparin-binding of the third Kunitz domain
of human tissue factor pathway inhibitor.";
Biochemistry 41:78-85(2002).
[16]
VARIANT MET-292.
MEDLINE=99318093; PubMed=10391209; DOI=10.1038/10290;
Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
Shaw N., Lane C.R., Lim E.-P., Kalyanaram N., Nemesh J., Ziaugra L.,
Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.G.,
Lander E.S.;
RA "Characterization of single-nucleotide polymorphisms in coding regions
of human genes.";
Nat. Genet. 22:231-238(1999).
[17]
RP
ERRATUM.
PubMed=10545957;
Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
Shaw N., Lane C.R., Lim E.-P., Kalyanaram N., Nemesh J., Ziaugra L.,
Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.G.,
Lander E.S.;
RA
Nat. Genet. 23:373-373(1999).
CC -I- FUNCTION: Inhibits factor X (X(a)) directly and, in a Xa-dependent
way, inhibits VIIa/tissue factor activity, presumably by forming a
quaternary Xa/LACI/VIIa/TF complex. It possesses an antithrombotic
action and also the ability to associate with lipoproteins in
plasma.
CC
-I- SUBCELLULAR LOCATION: Secreted.
CC
-I- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=Alpha; Synonyms=TFPIalpha;
IsoId=p10646-1; Sequence=Displayed;
Name=Beta; Synonyms=TFPIbeta;
IsoId=p10646-2; Sequence=VSP_003030, VSP_003031;
-I- TISSUE SPECIFICITY: Mostly in endothelial cells.
CC
-I- DOMAIN: This inhibitor contains three inhibitory domains. The
first domain interacts with VIIa and TF, the second one with Xa.
CC
-I- PTM: O-glycosylated.
CC
-I- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.

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between the Swiss Institute of Bioinformatics and the EMBL outstation
at the European Bioinformatics Institute. There are no restrictions on
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announcements
or send an email to license@isb-sib.ch).

EMBL: J03225; AAA52022.1; --
DR EMBL: M58650; AAA59480.1; --
DR EMBL: M58644; AAA59480.1; JOINED.
DR EMBL: M58645; AAA59480.1; JOINED.
DR EMBL: M58646; AAA59480.1; JOINED.
DR EMBL: M58647; AAA59480.1; JOINED.

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DR EMBL; M58648; AAA59480.1; JOINED.
DR EMBL; M58649; AAA59480.1; JOINED.

Query Match
Best Local Similarity 100.0%; Score 1528; DB 1; Length 304;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 29 DSEDEEHTITDTLPLPLKMHSCAFKADGPKAKMKRFFNIFTRQCEEFYGGCE 88
QY 61 GQNRFESLECKKCTRDNANRIKTTLOQEKDPFCFLEEDPGICRCGYITRYFYNNQTK 120
DB 89 GQNRFESLECKKCTRDNANRIKTTLOQEKDPFCFLEEDPGICRCGYITRYFYNNQTK 148
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DB 149 QCERFKYGGCLGNMNNFETLECKNICDGPNGFOVDNYGTQLNAVNNSLTPQSTKVPSL 208
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DB 209 FEHGPSWCLTPADRGCLCRANENFYNSVIGKCRPFKYSGCGGNNFTSKQECRLACK 268
QY 241 KGFTQRIKSGGLIKTKRKRKQKVIAEYEEFVKNM 276
DB 269 KGFTQRIKSGGLIKTKRKRKQKVIAEYEEFVKNM 304

RESULT 2
TFPI_MACMU
ID TFPI_MACMU STANDARD; PRT; 304 AA.
AC Q28864;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Tissue factor pathway inhibitor precursor (TFPI) (Lipoprotein-
DE associated coagulation inhibitor) (LACI) (Extrinsic pathway inhibitor)
DE (EPI).
GN Name=TFPI; Synonyms=TFPI1;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=94375417; PubMed=8089087;
RA Kamei S., Kanikubo Y., Hamuro T., Fujimoto H., Ishihara M.,
RA Yonemura H., Miyamoto S., Funatsu A., Enjiyoji K., Abumiya T.;
RT "Amino acid sequence and inhibitory activity of rhesus monkey tissue
RT factor pathway inhibitor (TFPI): comparison with human TFPI.";
RL J. Biochem. 115:708-714(1994).
CC -!- FUNCTION: Inhibits factor X (X(a)) directly and, in a Xa-dependent
CC way, inhibits VIIa/tissue factor activity, presumably by forming a
CC quaternary Xa/LACI/VIIa/TF complex. It possesses an antithrombotic
CC action and also the ability to associate with lipoproteins in
CC plasma.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DOMAIN: This inhibitor contains three inhibitory domains. The
CC first domain interacts with VIIa and TF, the second one with Xa
CC (By similarity).
CC -!- PTM: O-glycosylated (By similarity).
CC -!- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC

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EMBL; S73337; AAB31955.1; -.
DR PIR; JC2264; JC2264.
DR HSP; P10646; IIRH.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008296; TFPI.
DR Pfam; PF00014; Kunitz BPTI; 3.
DR PIRSF; PIRSF01620; TFPI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD00022; Prot_Inh_Kunz-m; 3.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 3.
KW Blood coagulation; Glycoprotein; Repeat; Serine protease inhibitor;
KW Signal.
FT SIGNAL 1 28 By similarity.
FT CHAIN 29 304 Tissue factor pathway inhibitor.
FT DOMAIN 54 104 BPTI/Kunitz inhibitor 1.
FT DOMAIN 125 175 BPTI/Kunitz inhibitor 2.
FT DOMAIN 217 267 BPTI/Kunitz inhibitor 3.
FT SITE 64 65 Reactive bond (By similarity).
FT SITE 135 136 Reactive bond (By similarity).
FT SITE 227 228 Reactive bond (By similarity).
FT DISULFID 54 104 By similarity.
FT DISULFID 63 87 By similarity.
FT DISULFID 79 100 By similarity.
FT DISULFID 125 175 By similarity.
FT DISULFID 134 158 By similarity.
FT DISULFID 150 171 By similarity.
FT DISULFID 217 267 By similarity.
FT DISULFID 226 250 By similarity.
FT DISULFID 242 263 By similarity.
FT CARBOHYD 145 145 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 195 195 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 256 256 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 304 AA; 35085 MW; 56E13B3FF16282B0 CRC64;

Query Match
Best Local Similarity 94.7%; Score 1447; DB 1; Length 304;
Matches 259; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 DSEDEEHTITDTLPLPLKMHSCAFKADGPKAKMKRFFNIFTRQCEEFYGGCE 60
DB 29 DSEDEEHTITDTLPLPLKMHSCAFKADGPKAKMKRFFNIFTRQCEEFYGGCE 88
QY 61 GQNRFESLECKKCTRDNANRIKTTLOQEKDPFCFLEEDPGICRCGYITRYFYNNQTK 120
DB 89 GQNRFESMECKKCTRDNANRIKTTLOQEKDPFCFLEEDPGICRCGYITRYFYNNQSK 148
QY 121 QCERFKYGGCLGNMNNFETLECKNICDGPNGFOVDNYGTQLNAVNNSLTPQSTKVPSL 180
DB 149 QCERFKYGGCLGNMNNFETLECKNICDGPNGFOVDNYGTQLNAVNNSLTPQSTKVPSP 208
QY 181 FEHGPSWCLTPADRGCLCRANENFYNSVIGKCRPFKYSGCGGNNFTSKQECRLACK 240
DB 209 FEHGPSWCLTPADRGCLCRANENFYNSVIGKCRPFKYSGCGGNNFTSKQECRLACK 268
QY 241 KGFTQRIKSGGLIKTKRKRKQKVIAEYEEFVKNM 276
DB 269 KGFTQRIKSGGLIKTKRKRKQKVIAEYEEFVKNM 304

RESULT 3
TFPI_RABIT
ID TFPI_RABIT STANDARD; PRT; 300 AA.
AC P19761; Q28828;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Tissue factor pathway inhibitor precursor (TFPI) (Lipoprotein-
DE associated coagulation inhibitor) (LACI) (Extrinsic pathway inhibitor)
DE (EPI).
GN Name=TFPI;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
[1]
SEQUENCE FROM N.A.
TISSUE=Liver;
MEDLINE=91057146; PubMed=2136251;
Wesselschmidt R.L., Girard T.J., Broze G.J. Jr.;
"cDNA sequence of rabbit lipoprotein-associated coagulation
inhibitor.";
Nucleic Acids Res. 18:6440-6440(1990).
[2]
REVISED: 72; 211 AND 218.
TISSUE=Liver;
MEDLINE=92335027; PubMed=1630940;
Warn-Granger B.J., Broze G.J. Jr., Komlives E.A.;
"cDNA sequence of rabbit tissue factor pathway inhibitor.";
Nucleic Acids Res. 20:3548-3548(1992).
[3]
SEQUENCE FROM N.A.
TISSUE=Lung;
MEDLINE=93276427; PubMed=85031133; DOI=10.1016/0049-3848(93)90059-W;
Belacouaj A., Kuppussawamy M.N., Birks J.J., Bajaj S.P.;
"Revised cDNA sequence of rabbit tissue factor pathway inhibitor.";
Thromb. Res. 69:547-553(1993).
-1- FUNCTION: Inhibits factor X (X(a)) directly and, in a Xa-dependent
way, inhibits VIIa/tissue factor activity, presumably by forming a
quaternary Xa/LACI/VIIa/TF complex. It possesses an antithrombotic
action and also the ability to associate with lipoproteins in
plasma.
-1- SUBCELLULAR LOCATION: Secreted.
-1- DOMAIN: This inhibitor contains three inhibitory domains. The
first domain interacts with VIIa and TF, the second one with Xa
(By similarity).
-1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.

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or send an email to license@isb-sib.ch).

EMBL; X54708; CAA38515.1; ALT_SEQ.
EMBL; S61902; AAB26836.1; -.
PIR; I46937; I46937.
HSPG; P10646; 1TFX.
InterPro; IPR002223; Prot_Inh_Kunz-m.
InterPro; IPR008296; TFPI.
Pfam; PF00014; Kunitz_BPTI; 3.
PRINTS; PRSF001620; TFPI; 1.
PRINTS; PR00759; BASICPTASE.
ProDom; PD000282; Prot_Inh_Kunz-m; 3.
PROSITE; PS00280; BPTI_KUNITZ_1; 3.
PROSITE; PS0279; BPTI_KUNITZ_2; 3.
Blood coagulation; Glycoprotein; Repeat; Serine protease inhibitor;
Signal.
Signal 1 24
CHAIN 25 300 Tissue factor pathway inhibitor.
DOMAIN 50 100 BPTI/Kunitz inhibitor 1.
DOMAIN 121 171 BPTI/Kunitz inhibitor 2.
DOMAIN 213 263 BPTI/Kunitz inhibitor 3.
SITE 60 61 Reactive bond (By similarity).
SITE 131 132 Reactive bond (By similarity).
SITE 223 224 Reactive bond (By similarity).
SITE 50 100 By similarity.
DISULFID 59 83 By similarity.
DISULFID 75 96 By similarity.
DISULFID 121 171 By similarity.
DISULFID 130 154 By similarity.
DISULFID 146 167 By similarity.
DISULFID 213 263 By similarity.
DISULFID 222 246 By similarity.


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DR InterPro: IPR008296; TPEI.
DR Pfam: PF00014; Kunitz_BPTI; 3.
DR PIRSF: PIRSF001620; TFEI; 1.
DR PRINTS: PR00759; BASICPFASE.
DR ProDom: PD000222; Prot_Inh_Kunz-m; 3.
DR SMART: SM00131; KU; 3.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE: PS0279; BPTI_KUNITZ_2; 3.
KW Hypothetical protein.
SQ SEQUENCE 287 AA; 33093 MW; DF69B3D76718115E CRC64;

Query Match 33.9%; Score 518; DB 2; Length 287;
Best Local Similarity 36.6%; Pred. No. 1.1e-35;
Matches 97; Conservative 48; Mismatches 78; Indels 42; Gaps 5;

Qy 19 LKLHSHFCADGPKADGPKAIMKRFNFTQCEEFYGGCGNQRNFESLECKMCTR 78
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
35 ITHFHSKALKKDEGPKALKDRFYDTGRCSEFYGGCGNQRNFETLQCEKMC- 92
Qy 79 DNANRIKTTLOQEKPDGCFLEEDPGICRGVITRYFYNNQTKOCERFYGGCGLNMMNPF 138
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
93 -----LVKEDKSPCLDDDEPGCRGLVPYFFDFKQCEKRFYGGCGFNANFK 142
Qy 139 TLEECKNICEDGPNQFGQ-----VDNYGTQLNAVNV---NSLTPOSTK 176
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
143 TIKECHERCLPALNNMERNAPLKPEEBAKPKTEPLAKHVEAPLNASHLPNQRKSPSAK 202
Qy 177 VPSLFEFHGPGSWCLTPADRGILCRANENRFFYNVIGKCRPFYGGCGNQRNFSTKQRECL 236
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
203 KPRL---NRPKLCFSPIDRGNCSEGRYMYNPRTKRCQMFHYSGCGNKNFVKRGDCI 259
Qy 237 RACKGFTQRIKSGGLIKTKRK 261
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
260 KCMRDLRRK-----LIRLKLRSK 279

RESULT 11
Q7T025 ID Q7T025 PRELIMINARY; PRT; 224 AA.
AC Q7T025;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MGC68843 protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Alcega S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences".
RP Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
initiative.";
RL Dev. Dyn. 225:384-391 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
Klein S., Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.
DR EMBL; BC055972; AAH55972.1; -.
DR HSSP; P00974; 1BPI.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro: IPR002223; F:serine-type endopeptidase inhibitor activity; IEA.
DR Pfam; PF00014; Kunitz_BPTI; 3.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 3.
DR SMART; SM00131; KU; 3.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 3.
SQ SEQUENCE 224 AA; 25538 MW; 11C2D1C4C789445B CRC64;

Query Match 30.3%; Score 463; DB 2; Length 224;
Best Local Similarity 36.5%; Pred. No. 3.7e-31;
Matches 91; Conservative 34; Mismatches 68; Indels 56; Gaps 6;

Qy 18 PLKLHSHFCADGPKADGPKAIMKRFNFTQCEEFYGGCGNQRNFESLECKMCTR 77
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
22 PMQGNVTVCLLPLDEGPKALIPHYYDYRYTQCEFYGGCGNQRNFVSMEDCEKFCW 81
Qy 78 RDANRIKTTLOQEKPDGCFLEEDPGICRGVITRYFYNNQTKOCERFYGGCGLNMMNPF 137
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
82 K-----LK-----KVPKACRMVDEGFCRGYIKRYANMKTMRCEQFIYGGCYGNDNF 130
Qy 138 ETLSECKNICEDGPNQFGQVDNYGTQLNAVNVSLTPQSTKVPSPSLFEFHGPGSWCLTPADRG 197
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
131 QDKDCINFC-----APRR-----DAPSPCYSPKDEGS 158
Qy 198 CRANENRFFYNVIGKCRPFYGGCGNQRNFSTKQRECLRACKGFTQRIKSGGLIKTKR 257
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
159 CSASVTTRYFYFNIESKACEEFYTGCGNSNNFIKVEDCDSCYCKKG-----TKR 206
Qy 258 KRKKQKRVKI 266
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
207 PR-NQNPXI 214

RESULT 12
Q8AVE1 ID Q8AVE1 PRELIMINARY; PRT; 277 AA.
AC Q8AVE1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tissue factor pathway inhibitor.
GN Namestfpia;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Hanumanthaiah R., Day K., Jagadeeswaran P.;
RT "Comprehensive analysis of blood coagulation pathways in teleostei:
Evolution of coagulation factor genes and identification of zebrafish
factor VIII.";
RL Blood Cells Mol. Dis. 0:0-0 (2002).
CC -!- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
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DR EMBL; AF515274; AAN71004.1; -.
DR HSSP; P31713; 1SHP.
DR ZFIN; ZDB-GENE-030711-1; tipia.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0030414; F:protease inhibitor activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008296; TFPI.
DR Pfam; PF00014; Kunitz BPTI; 3.
DR PIRSF; PIRSF001620; TFPI; 1.
DR PRINTS; PRO0759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 3.
DR SMART; SM00131; KU; 2.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 2.
SQ SEQUENCE 277 AA; 31942 MW; 0F68F0EAEF9B100F CRC64;

Query Match 29.2%; Score 446; DB 2; Length 277;
Best Local Similarity 31.4%; Pred. No. 1.3e-29;
Matches 86; Conservative 58; Mismatches 84; Indels 46; Gaps 5;

QY 19 LKLMHSCAFKADGCPCKAIMKRFNFITRQCEFIYGGCEGNONRFESLEECCKMCTR 78
DB 34 LRIFHQSCALRDEGCPCKAMKRDYFDIDTCRCEPFYGGCGGNANNFETLQDCCEMC-- 91
QY 79 DNANRIKTTILOQKPDFCFLEEDPGICRGYITRYFYNNQTKQCERFYGGCLGNMNF 138
DB 92 -----LVTENKSFCHLEDEPGCPGLVPYFFDQKQCEKQFYGGCFGNANFK 141
QY 139 TLECKNICE-----DGPNGFQVDNYGTQLNAVNSLTPSTKVPSLFE 182
DB 142 TIKACQRCOLTAVLKSEEEBAKVPESP-----AIHDDAHLNSSHLSALSRVFPQKQAE 197
QY 183 FHGSPSWCLTPADRGICRANERFYNSVIGKCRPKYGGCGGNENFTSKOECILRACKG 242
DB 198 FSPPELMSAVDRGDCGSEERYVFNPRIGQCQVR-SLDVEQQLHPORHCKMNC--- 253
QY 243 FQIRISKGLIKTRKKRKQKVIAEYEIFVKNM 276
DB 254 -----MKDQHRKQIRIKTNSNLPFSV 277

RESULT 13
QY 81T91 PRELIMINARY; PRT; 759 AA.
AC Q81T91;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
OS Kunitz-like protease inhibitor precursor.
OC Ancylostoma caninum (Dog hookworm).
OC Eukaryota; Metazoa; Nematoda; Chordata; Rhabditida; Strongylida;
OC Ancylostomatidae; Ancylostomatidae; Ancylostominae; Ancylostoma.
OX NCBI_TaxID=23170;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=Baltime;
RX MEDLINE=22645137; PubMed=12760667;
RA Hawdon J.M., Datu B., Crowell M.;
RT "Molecular cloning of a novel multidomain Kunitz-type proteinase
inhibitor from the hookworm Ancylostoma caninum.";
RL J. Parasitol. 89:402-407(2003).
CC -1- SIMILARITY: Contains 12 BPTI/Kunitz inhibitor domains.
DR EMBL; AF533590; AAN10061.1; -.
DR HSSP; P31713; 1SHP.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz BPTI; 12.
DR PRINTS; SM00131; KU; 12.
DR SMART; PS00280; BPTI_KUNITZ_1; 10.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 10.

DR PROSITE; PS50279; BPTI_KUNITZ_2; 12.
KW Protease; Signal. 16 Potential.
FT SIGNAL 759 AA; 84886 MW; C43IA3C3F418F40A CRC64;
SQ SEQUENCE 759 AA; 84886 MW; C43IA3C3F418F40A CRC64;

Query Match 27.1%; Score 414.5; DB 2; Length 759;
Best Local Similarity 33.6%; Pred. No. 1.9e-26;
Matches 97; Conservative 33; Mismatches 106; Indels 53; Gaps 6;

QY 3 EDEEHTIITDELPPLKLMHSCAFKADGCPCKAIMKRFNFITRQCEFIYGGCEGN 62
DB 370 ESMEECTRTCKAVPEPEPEKETCSQPIEVGCPCKAMKRYAYDNKKNKCVRFYGGCKGN 429
QY 63 QNRFESLEECCKMCTRDNANRIKTTILOQKPDFCFLEEDPGICRGYITRYFYNNQTKQ 122
DB 430 KNFESMEECTRT-----KKAVPEPEQDTCSQPIEVGCPCKAMKRYAYDNKKNK 480
QY 123 ERKYGGCLGNMNFETLECKNIC-----EDGP-----NGFQVDN- 158
DB 481 VRFYGGCKGNKNFESMEECTRTCKKAVPEPEPEKETCSQPIEAGCKAVRFAVDNA 540
QY 159 -----YGTQLNAVNSLT-----POSTKVPSLFPHGSPSWCLTPADRGICRANE 202
DB 541 KEKCEVEFFYGGCKGNKNFETMEDCTFTCQRLAKPELEK-----DVCSPITAGFCRA 596
QY 203 NRFYNSVIGKCRPKYGGCGGNENFTSKOECILRACKGFIQIRISKG 251
DB 597 PRGYDSKKRCKVKFYGGCKGNRFPYTNKECEKTCRGATGTTNPGG 645

RESULT 14
QY 81T91 PRELIMINARY; PRT; 234 AA.
AC QY81T91;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
OS Tissue factor pathway inhibitor-2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RC SEQUENCE FROM N.A.
RP MEDLINE=22802738; PubMed=12921785; DOI=10.1016/S0003-9861(03)00332-1;
RX Du X., Deng F.M., Chand H.S., Kisiel W.;
RA "Molecular cloning, expression, and characterization of bovine tissue
factor pathway inhibitor-2.";
RL Arch. Biochem. Biophys. 417:96-104(2003).
RN [2]
RC SEQUENCE FROM N.A.
RP Deng F.-M., Kisiel W., Sun T.-T.;
RA Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RL -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.
CC EMBL; AY234861; AAO84035.1; -.
DR HSSP; P00981; 1DTK.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz BPTI; 3.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 3.
DR SMART; SM00131; KU; 3.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 3.
SQ SEQUENCE 234 AA; 26675 MW; 401EEC84D589B422 CRC64;

Query Match 25.7%; Score 392; DB 2; Length 234;
Best Local Similarity 29.3%; Pred. No. 3.9e-25;
Matches 78; Conservative 41; Mismatches 93; Indels 54; Gaps 4;

QY 9 TIITDELPPLKLMHSCAFKADGCPCKAIMKRFNFITRQCEFIYGGCEGNONRFES 68
DB 19 TALGDASQAPPGNNAEICLLPDDGFCRARISFYDYRTQSCREFMYGGCEGNANFET 78

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 16, 2005, 03:17:23 ; Search time 44 Seconds
(without alignments)
603.542 Million cell updates/sec

Title: US-10-753-079-1
Perfect score: 1528
Sequence: 1 DSEDEDEHTITDTELPPLK.....RRKKQKVKIAYEIVFKNM 276

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1528	100.0	304	1	TIHUGK
2	1447	94.7	304	1	JC2264
3	1124	73.6	299	2	I46937
4	1112	72.8	300	2	S12143
5	993	65.0	396	2	S53325
6	934.5	61.2	302	1	TIRTKK
7	384.5	25.2	235	2	A54951
8	355.5	23.3	1558	2	C89114
9	335.5	23.3	2167	2	T34395
10	350.5	22.9	2225	2	T26063
11	347	22.7	1474	2	D88550
12	340	22.3	922	2	T23573
13	334.5	21.9	1522	2	H88380
14	332.5	21.8	1416	2	E88550
15	332.5	21.8	2844	2	S28291
16	327	21.4	1599	2	T16210
17	309	20.2	1965	2	T33216
18	303	19.8	1391	2	T20406
19	302.5	19.8	1743	2	T26859
20	296.5	19.4	1043	2	T19734
21	253	16.6	838	2	T20125
22	252.5	16.5	1203	1	T21275
23	240.5	15.7	352	1	HCHU
24	239	15.6	125	1	TIHOBI
25	238	15.6	123	2	A29652
26	236	15.4	22	2	JG0185
27	233	15.2	1208	2	T27822
28	232.5	15.2	352	1	TIHOBI
29	229	15.0	337	1	TIIPGI

30	225.5	14.8	349	2	S21089
31	223	14.6	349	2	S35708
32	220.5	14.4	692	2	T32980
33	199	13.0	372	2	JC2556
34	196.5	12.9	355	1	S22181
35	190.5	12.5	805	2	T34212
36	189.5	12.4	183	2	T28711
37	189	12.4	65	1	TIIVVC
38	183	12.0	61	1	TIIVTI
39	183	12.0	62	2	S19327
40	176	11.5	62	2	A44180
41	175.5	11.5	110	1	TIITOR
42	172	11.3	67	1	TIBOC
43	170	11.1	219	2	T21736
44	169	11.1	58	1	TIHABK
45	169	11.1	60	1	TIIVRV2

ALIGNMENTS

RESULT 1

TIHUGK

tissue factor pathway inhibitor precursor [validated] - human

N:Alternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation inhib

C:Species: Homo sapiens (man)

C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text change 09-Jul-2004

C/Accession: A23712; A39176; A28650; A60433; B60433; S13034; A34315; A38294; S03903

R/Girard, T.J.; Eddy, R.; Wesselschmidt, R.L.; MacPhail, L.A.; Likert, K.M.; Byers, M.G

J. Biol. Chem. 266, 5036-5041, 1991

A:Title: Structure of the human lipoprotein-associated coagulation inhibitor gene. Intro

A:Reference number: A23712; MUID:91161593; PMID:2002045

A/Accession: A23712

A/Molecule type: DNA

A/Residues: 1-304 <GIR>

A/Cross-references: UNIPROT:P10646; GB:M59493; GB:M59499; NID:g187204; PIDN:AAA59536.1;

R:van der Logt, C.P.E.; Reitsma, P.H.; Bertina, R.M.

Biochemistry 30, 1571-1577, 1991

A:Title: Intron-exon organization of the human gene coding for the lipoprotein-associated

A:Reference number: A39176; MUID:91129227; PMID:1993173

A/Accession: A39176

A/Molecule type: DNA

A/Residues: 1-304 <VAN>

A/Cross-references: GB:M58650; GB:J05312; NID:g186827; PIDN:AAA59480.1; PID:g186829

R:Wun, T.C.; Kretzmer, K.K.; Girard, T.J.; Miletich, J.P.; Broze Jr., G.J.

J. Biol. Chem. 263, 6001-6004, 1988

A:Title: Cloning and characterization of a cDNA coding for the lipoprotein-associated co

A:Reference number: A28650; MUID:88198127; PMID:2452157

A/Accession: A28650

A/Molecule type: mRNA

A/Residues: 1-304 <WUN>

A/Cross-references: GB:J03225; NID:g180545; PIDN:AAA52022.1; PID:g180546

A:Note: part of this sequence, including the amino end of the mature protein, was confil

R/Girard, T.J.; Warren, L.A.; Novotny, W.F.; Bejcek, B.E.; Miletich, J.P.; Broze Jr., G.

Thromb. Res. 55, 37-50, 1989

A:Title: Identification of the 1.4 KB and 4.0 KB messages for the lipoprotein associated

A:Reference number: A60433; MUID:89388722; PMID:2781520

A/Accession: A60433

A/Molecule type: mRNA

A/Status: not compared with conceptual translation

A/Residues: 1-304 <GI2>

A/Experimental source: endothelial cells

A/Accession: B60433

A/Molecule type: protein

A/Residues: 'XX', 31-53, 'X', 55-56 <GI3>

A:Experimental source: recombinant material from mouse C137 cells

R/Girard, T.J.; McCourt, D.; Novotny, W.F.; MacPhail, L.A.; Likert, K.M.; Broze Jr., G.J

Biochem. J. 270, 621-625, 1990

A:Title: Endogenous phosphorylation of the lipoprotein-associated coagulation inhibitor

A:Reference number: S13034; MUID:91054349; PMID:2122883

A/Accession: S13034

A/Molecule type: protein

A/Residues: 29-35 <GI4>

R;Novotny, W.F.; Girard, T.J.; Miletich, J.P.; Broze Jr., G.J.
J. Biol. Chem. 264, 18832-18837, 1989
A;Title: Purification and characterization of the lipoprotein-associated coagulation inhibitor
A;Reference number: A34315; MUID:90036996; PMID:2553722
A;Accession: A34315
A;Molecule type: protein
A;Residues: 'XX', 31-33, 'L', 35-50 <NOV>
A;Experimental source: plasma
R;Pedersen, A.H.; Nordfang, O.; Norris, F.; Wiberg, F.C.; Christensen, P.M.; Moeller, K.
J. Biol. Chem. 265, 16786-16793, 1990
A;Title: Recombinant human extrinsic pathway inhibitor. Production, isolation, and characterization
A;Reference number: A38294; MUID:91009092; PMID:2211593
A;Accession: A38294
A;Molecule type: protein
A;Residues: 29-41 <PEB>
R;Girard, T.J.; Warren, L.A.; Novotny, W.F.; Likert, K.M.; Brown, S.G.; Miletich, J.P.; Nature 338, 518-520, 1989
A;Title: Functional significance of the Kunitz-type inhibitory domains of lipoproteinase-A
A;Reference number: S03903; MUID:89181950; PMID:2927510
A;Contents: annotation; site-directed mutagenesis
C;Comment: The first Kunitz-type domain binds the factor VIIa/tissue factor complex; the
C;Genetics:
A;Gene: GDB:TFPI
A;Cross-references: GDB:127364; OMIM:152310
A;Map position: 2q32-2q32
A;Introns: 41/1; 107/1; 120/1; 179/1; 210/1; 270/1
C;Function:
A;Description: regulates clotting by factor Xa-dependent inhibition of the coagulation factor
A;Pathway: blood coagulation
C;Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
C;Keywords: anticoagulant; blood coagulation; duplication; glycoprotein; heparin binding
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-304/Product: tissue factor pathway inhibitor #status experimental <MAT>
F;54-104/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F;125-175/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F;217-267/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>
F;54-104/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F;125-175/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F;217-267/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>
F;284-289/Region: heparin binding #status predicted
F;30/Binding site: phosphate (Ser) (covalent) #status experimental
F;54-104, 63-87, 79-100, 125-175, 134-158, 150-171, 217-267, 226-250, 242-263/Disulfide bonds: #
F;64/Inhibitory site: Lys (coagulation factor VII/tissue factor complex) #status experimental
F;135/Inhibitory site: Arg (coagulation factor X) #status experimental
F;145, 195, 256/Binding site: carboxylate (Asn) (covalent) #status predicted
F;227/Inhibitory site: Arg (unidentified proteinase) #status predicted

Query Match 100.0%; Score 1528; DB 1; Length 304;
Best Local Similarity 100.0%; Pred. No. 8.9e-118;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSEDEHTIITDTLPPLKLMHSFCAPKADGCKAIMKRFNFTTQCEEFYGGCE 60
Db 29 DSEDEHTIITDTLPPLKLMHSFCAPKADGCKAIMKRFNFTTQCEEFYGGCE 88

Qy 61 GNQRFPSLECKKMCCTRDNANRIKTTLOQKDPDFCFLEDPGICRGYITRYFNNQTK 120
Db 89 GNQRFPSLECKKMCCTRDNANRIKTTLOQKDPDFCFLEDPGICRGYITRYFNNQTK 148

Qy 121 QCERFKYGGCLGNMNNFETLECKNICEDGPNQFQVDNYGTQLNANNSLTTPQSTKVPSSL 180
Db 149 QCERFKYGGCLGNMNNFETLECKNICEDGPNQFQVDNYGTQLNANNSLTTPQSTKVPSSL 208

Qy 181 FEHGPSWCLTPADRGICLANENRFFYNSVIGKCRPPKSYCGCGNENFTSKQCLRACK 240
Db 209 FEHGPSWCLTPADRGICLANENRFFYNSVIGKCRPPKSYCGCGNENFTSKQCLRACK 268

Qy 241 KGFIQRIKSGGLIKTKRKKQKVIAEYEFVKNM 276
Db 269 KGFIQRIKSGGLIKTKRKKQKVIAEYEFVKNM 304

RESULT 2
JC2264
tissue factor pathway inhibitor precursor - rhesus macaque
N;Alternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation inhib

C;Species: Macaca mulatta (rhesus macaque)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JC2264
R;Kamei, S.; Kamikubo, Y.; Hamuro, T.; Fujimoto, H.; Ishihara, M.; Yonemura, H.; Miyamoto, J. Biochem. 115, 708-714, 1994
A;Title: Amino acid sequence and inhibitory activity of rhesus monkey tissue factor pathway inhibitor
A;Reference number: JC2264; MUID:94375417; PMID:8089087
A;Accession: JC2264
A;Molecule type: mRNA
A;Residues: 1-304 <KAM>
A;Cross-references: UNIPROT:Q28864; GB:S73337; NID:G685016; PIDN:AAB31955.1; PID:G685017
A;Experimental source: liver
C;Comment: This protein inhibits the activities of factor Xa and tissue factor-VI
C;Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
C;Keywords: anticoagulant; glycoprotein; serine proteinase inhibitor
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-304/Product: tissue factor pathway inhibitor #status predicted <MAT>
F;54-104/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F;125-175/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F;217-267/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>
F;54-104, 63-87, 79-100, 125-175, 134-158, 150-171, 217-267, 226-250, 242-263/Disulfide bonds: #
F;64/Inhibitory site: Lys (coagulation factor VII/tissue factor complex) #status predicted
F;135/Inhibitory site: Arg (coagulation factor X) #status predicted
F;145, 195, 256/Binding site: carboxylate (Asn) (covalent) #status predicted
F;227/Inhibitory site: Arg (unidentified proteinase) #status predicted

Query Match 94.7%; Score 1447; DB 1; Length 304;
Best Local Similarity 93.8%; Pred. No. 3.8e-111;
Matches 259; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DSEDEHTIITDTLPPLKLMHSFCAPKADGCKAIMKRFNFTTQCEEFYGGCE 60
Db 29 DSEDEHTIITDTLPPLKLMHSFCAPKADGCKAIMKRFNFTTQCEEFYGGCE 88

Qy 61 GNQRFPSLECKKMCCTRDNANRIKTTLOQKDPDFCFLEDPGICRGYITRYFNNQTK 120
Db 89 GNQRFPSLECKKMCCTRDNANRIKTTLOQKDPDFCFLEDPGICRGYITRYFNNQTK 148

Qy 121 QCERFKYGGCLGNMNNFETLECKNICEDGPNQFQVDNYGTQLNANNSLTTPQSTKVPSSL 180
Db 149 QCERFKYGGCLGNMNNFETLECKNICEDGPNQFQVDNYGTQLNANNSLTTPQSTKVPSSL 208

Qy 181 FEHGPSWCLTPADRGICLANENRFFYNSVIGKCRPPKSYCGCGNENFTSKQCLRACK 240
Db 209 FEHGPSWCLTPADRGICLANENRFFYNSVIGKCRPPKSYCGCGNENFTSKQCLRACK 268

Qy 241 KGFIQRIKSGGLIKTKRKKQKVIAEYEFVKNM 276
Db 269 KGFIQRIKSGGLIKTKRKKQKVIAEYEFVKNM 304

RESULT 3
I46937
tissue factor pathway inhibitor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
C;Accession: I46937
R;Belasouaj, A.; Kuppussawmy, M.N.; Birktoft, J.J.; Bajaj, S.P. Thromb. Res. 69, 547-553, 1993
A;Title: Revised cDNA sequence of rabbit tissue factor pathway inhibitor.
A;Reference number: I46937; MUID:93276427; PMID:8503123
A;Accession: I46937
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-299 <BEL>
A;Cross-references: UNIPROT:P19761; GB:S61902; NID:G386015; PIDN:AAB26836.1; PID:G386016
C;Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
F;49-99/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F;120-170/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F;212-262/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>

Query Match 73.6%; Score 1124; DB 2; Length 299;
Best Local Similarity 73.4%; Pred. No. 1e-84;

Matches	199;	Conservative	26;	Mismatches	46;	Indels	0;	Gaps	0;
Qy	4	EEDEHTIITDELPLKLMSFCFAKADDPCKAIKMRFFNFITRQCEEFYGGCEG	63						
Db	27	EEDEFTNITDKPLQKPTHSFCAMKVDDGPCRAYIKRFFNFILTHQCEEFYGGCEG	86						
Qy	64	NRPFESLECKKMCRTDNANRIIKTTLQEKDPDFCFLEEDPGICRGYITRYFYNNQKCE	123						
Db	87	NRPFESLECKKCARDYPKMTTKLTFOGKDPDFCFLEEDPGICRGYITRYFYNNQKCE	146						
Qy	124	RFKYGGCLGNMNFETLECKNICEDGPNQVDNYGTQLNANVNSLTPOSTKVPSLPEF	183						
Db	147	RFKYGGCLGNMNFESLECKNCTCENTSFQVDDHRTQLTNTVNTLINOPTKAPRWAF	206						
Qy	184	HGPSWCLTPADRGICRANENRFYNSVIGKRPFKYSGCGNENNFSTKQELRACKKG	243						
Db	207	HGPSWCLPPADRGICQANEIRFFYNAIIGKRPFKYSGCGNENNFSTKACITACKKG	266						
Qy	244	IQRISKGLIKTKRKXKQKVATAYEIFVK	274						
Db	267	IRNLSKGLIKTKRKKXQPKVITYVETFK	297						

RESULT 4

S12143

lipoprotein-associated coagulation inhibitor precursor - rabbit

N;Alternate names: endothelial cell coagulation inhibitor; endothelial cell tissue factor

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999

C;Accession: S12143; A61373

R;Wesselschmidt, R.L.; Girard, T.J.; Broze Jr., G.J.

Nucleic Acids Res. 18, 6440, 1990

A;Title: cDNA sequence of rabbit lipoprotein-associated coagulation inhibitor.

A;Reference number: S12143; MUID:91057146; PMID:2136251

A;Accession: S12143

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-300 <WES>

A;Cross-references: EMBL:X54708; NID:g1612; PIDN:CAA38515.1; PID:g1613

R;Colburn, P.; Crabb, J.W.; Buonassisi, V.

J. Cell. Physiol. 148, 320-326, 1991

A;Title: Enhanced inhibition of tissue factor by the extended form of an endothelial cell

A;Reference number: A61373; MUID:91349227; PMID:1890157

A;Accession: A61373

A;Molecule type: protein

A;Residues: 25-33,'X',35-46 <COL>

C;Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor

C;Keywords: anticoagulant; glycoprotein

F;50-100/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>

F;121-171/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>

F;213-263/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>

Query Match 72.8%; Score 1112; DB 2; Length 300;

Best Local Similarity 72.5%; Pred. No. 1e-83;

Matches 198; Conservative 25; Mismatches 50; Indels 0; Gaps 0;

Qy	2	SEDEEHTITDTLPLKLMSFCFAKADDPCKAIKMRFFNFITRQCEEFYGGCEG	61						
Db	26	AEDDEEFTNITDKPLQKPTHSFCAMKVDDGPCRAYIKRFFNFILTHQCEEFYGGCEG	85						
Qy	62	NONRFESLECKKMCRTDNANRIIKTTLQEKDPDFCFLEEDPGICRGYITRYFYNNQTK	121						
Db	86	NEINFESLECKKCARDYPKMTTKLTFOGKDPDFCFLEEDPGICRGYITRYFYNNQSKQ	145						
Qy	122	CERFKYGGCLGNMNFETLECKNICEDGPNQVDNYGTQLNANVNSLTPOSTKVPSLPF	181						
Db	146	CERFKYGGCLGNMNFESLECKNCTCENTSFQVDDHRTQLTNTVNTLINOPTKAPRW	205						
Qy	182	EFHGPSWCLTPADRGICRANENRFYNSVIGKRPFKYSGCGNENNFSTKQELRACKK	241						
Db	206	AFHGPSWCLPPADRGICQANEIRFFYNAIIGKRPFKYSGCGNENNFSTKACITACKK	265						
Qy	242	GFIORISKGLIKTKRKXKQKVATAYEIFVK	274						

```

Db      266 GFIPKSIKGGLIKTKRKKKQPKVITYVFVK 298
      ||| : ||||| ||| ||| ||| ||| |||
RESULT 5
S53325
tissue factor pathway inhibitor - rabbit
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 17-Mar-2003
C/Accession: S53325
R/Girard, T.J.; Gallani, D.; Broze Jr., G.J.
Biochem. J. 303, 923-928, 1994
A/Title: Complementary DNA sequencing of canine tissue factor pathway inhibitor reveals
A/Reference number: S53325; MUID:95071310; PMID:7980463
A/Accession: S53325
A/Status: preliminary
A/Molecule type: mRNA
A/Molecule type: 1-396 <GIR>
A/Residues: 1-396 <GIR>
C/Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
C/Keywords: serine proteinase inhibitor
F:53-103/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F:125-175/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F:309-359/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>

Query Match          55.0%; Score 993; DB 2; Length 396;
Best Local Similarity 51.8%; Pred. No. 7.5e-74;
Matches 191; Conservative 36; Mismatches 44; Indels 98; Gaps 6;

Qy    3 EDEEHTIITDTELPLKLHMSFCAPKADDPCKAIKRPFENIFTRQCBEFIYGCCEGN 62
      : ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db    31 DEEEYPGITD-ELPURLLHSPCALKDADGPCRAMIRNYFFNIHQCCBEFIYGCCEGN 89
      : ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy    63 QNRPESLEECKCMCTRONANRIKT-TLOQ--EKPDFCFLEEDPGICRGYITRYFYNNQT 119
      : ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db    90 QNRPESEECCEKCVRVPK--AKTELEKVLKPDYCHNEDSGLCRGFTVTRYNNVS 147
      : ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy    120 QKERFKYGCGCLGMNNFETLECKNICE----- 148
      : ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db    148 SKCEGFYGGCLGNLNNFETLEQCKNTCEGSIDLLMDETNNVTGSPGMNNTSLFNSGDS 207
      : ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy    149 -----DGP 151
      : ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db    208 LLPADSDGSMPPDSEIGGLQHDSSEGLQHDSSEGLQHDSSEGLQHDSSEGLQHDSSE 267
      : ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy    152 NG----FQVDNYGTQLNAVNSLTPOSTKVPSLFEFHGPGSWCLTPDRGLCRANENRFYY 207
      : ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db    268 SGGLQHDSGDNTSPVSVNNDSTFRPTTVSSFLFYGPSWCLTPDRGLCHANESRFYY 327
      : ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy    208 NSVI GKCRPFYSGCGGNENFTSKOECLACKKGFTQRISKGGLIKTKRKRRKKQRVKIA 267
      : ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db    328 NSVI GKCRPFYSGCGGNENFTSKACLTACKKGFMRISKGGLIKTKRKRRKKQTVKIV 387
      : ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy    268 YEIEFVKQM 276
      : ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db    388 YEKIFVKKL 396
      : ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6
TIRTGK
tissue factor pathway inhibitor precursor - rat
N/Alternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation inhibi
C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: JX0213
R:Enryoji, K.; Emi, M.; Mukai, T.; Kato, H.
J. Biochem. 111, 681-687, 1992
A/Title: cDNA cloning and expression of rat tissue factor pathway inhibitor (TFPI).
A/Reference number: JX0213; MUID:92348361; PMID:1639767
A/Accession: JX0213
A/Molecule type: mRNA
A/Residues: 1-302 <ENU>
A/Cross-references: UNIPROT:Q02445; DDBJ:D10926; NID:G220916; PID:BAA01724.1; PTD:G2209
A/Experimental source: liver
```


Qy 77 ---TRDNANR-----IIKTLQKEP-----DFCFLEEDPG 104
Db 1323 FVHGQPSAAQEQAPAAQAPQAPQAGNIIVSPQOSASPVVPSNSKQRDACHLNVDDG 1362
Qy 105 ICRGYITRYFYNNOTKQERFKYGGCLGNMNFETLECKNICE-----DGNG 153
Db 1383 RCKGAFDSWYEVATGSCVTFKYTGCGGNANRFASKQDCESLCVKPASEAASAGIDGAAG 1442
Qy 154 FOVDNYGQLNAVNNLSLPQSTKVPSLFEFHGSPSWCLTPADRGLCRANENRFYNSVIGK 213
Db 1443 -----INSV-----CDEAKDTGPTCTNFTVTKWYNKADGT 1471
Qy 214 CRPFKYSCGGNENFTSKQECRLACK 240
Db 1472 CNRFHYGCGQGNRNFDFNEQCKAACQ 1498
RESULT 9
T34395
hypotheical protein C37C3.6b - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T34395
R:Geisel, C.; Bradshaw, H.
submitted to the EMBL Data Library, July 1996
A:Description: The sequence of C. elegans cosmid C37C3.
A:Reference number: 221518
A:Accession: T34395
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-2167 <GBI>
A:Cross-references: UNIPROT:O76840; EMBL:U64857; PIDN:AAC25868.1; GSPDB:GN00023; CESP:C37C3.6a
A:Experimental source: strain Bristol N2; clone C37C3
A:Accession: T34394
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-1555, 'SKP' <GB2>
A:Cross-references: EMBL:U64857; PIDN:AAC25867.1; GSPDB:GN00023; CESP:C37C3.6a
A:Experimental source: strain Bristol N2; clone C37C3
C:Genetics:
A:Gene: CESP:C37C3.6b; CESP:C37C3.6a
A:Map position: 5
A:Introns: 32/3; 104/2; 156/2; 207/1; 459/2; 536/3; 577/2; 1105/3; 1367/1; 1438/1; 1556/

Query Match 23.3%; Score 355.5; DB 2; Length 2167;
Best Local Similarity 28.8%; Pred. No. 7.4e-21;
Matches 77; Conservative 32; Mismatches 83; Indels 75; Gaps 6;
Qy 18 PLKLMHSCAFKADGPKCAIMKRFNIFTRQCEFIYGGCGNQRNFESLECKKMC- 76
Db 1263 PRQSMEDICRSQDAGPCETYSDFWYNAFQCEBTFTYGGCGNLNFRSKDECEQRCF 1322
Qy 77 ---TRDNANR-----IIKTLQKEP-----DFCFLEEDPG 104
Db 1323 FVHGQPSAAQEQAPAAQAPQAPQAGNIIVSPQOSASPVVPSNSKQRDACHLNVDDG 1362
Qy 105 ICRGYITRYFYNNOTKQERFKYGGCLGNMNFETLECKNICE-----DGNG 153
Db 1383 RCKGAFDSWYEVATGSCVTFKYTGCGGNANRFASKQDCESLCVKPASEAASAGIDGAAG 1442
Qy 154 FOVDNYGQLNAVNNLSLPQSTKVPSLFEFHGSPSWCLTPADRGLCRANENRFYNSVIGK 213
Db 1443 -----INSV-----CDEAKDTGPTCTNFTVTKWYNKADGT 1471
Qy 214 CRPFKYSCGGNENFTSKQECRLACK 240
Db 1472 CNRFHYGCGQGNRNFDFNEQCKAACQ 1498
RESULT 10
T26063
hypotheical protein w01f3.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26063
R:Cummings, P.
submitted to the EMBL Data Library, March 1997
A:Reference number: 220145
A:Accession: T26063
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-2225 <WIL>
A:Cross-references: UNIPROT:O45881; EMBL:Z92815; PIDN:CAB07294.1; GSPDB:GN00023; CESP:W01F3
A:Experimental source: clone W01F3
C:Genetics:
A:Gene: CESP:W01F3.3
A:Map position: 5
A:Introns: 33/1; 56/1; 100/1; 142/3; 271/3; 451/1; 525/3; 774/1; 1093/1; 1178/1; 1221/1;
Query Match 22.9%; Score 350.5; DB 2; Length 2225;
Best Local Similarity 29.6%; Pred. No. 2e-20;
Matches 79; Conservative 32; Mismatches 91; Indels 65; Gaps 7;
Qy 1 DSEEDDEHIIITDTE-----LPPLKLMHSF-----CAFKADGQPC 35
Db 727 DEEESEVVEEQEDGKEEPLHVQPEVSQONTVLLGGIEDTTTDSVNRCLHPRDSGNC 786
Qy 36 KAIMKRPFFNIFTRQCEFIYGGCGNQRNFESLECKMCTRDNANRIITLQKEKPD 95
Db 787 RGQFVRWFFDDEKKNCDVFTYTGCGGNFASKEECMAICHKPEPT-----PSATPD 839
Qy 96 F---CFLEEDPGICRGVITRYFYNNOTKQERFKYGGCLGNMNFETLECKNICEDEGPN 152
Db 840 PSQVCSNDVDAGECNGVFERPAPDAEQDCRAFTYGGCGGNFATWQECRSRC----- 894
Qy 153 GFQVDNYGTQLNAVNNLSLPQSTKVPSLFEFHGSPSWCLTPADRGLCRANENRFYNSVIG 212
Db 895 -----VWAMKKS--PVAT-----CEADIEVGEBCAGVFSRFAFDKSGIN 929
Qy 213 KCRPFKYSCGGNENFTSKQECRLAC 239
Db 930 ACSFTYGGCGGNANFATLQECTNKC 956
RESULT 11
D88550
protein ZC84.6 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: D88550
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C.ele
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: D88550
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1474 <STO>
A:Cross-references: UNIPROT:O62504; GB:chr_III; PIDN:CAA79570.1; PID:g3881447; GSPDB:GN0
C:Genetics:
A:Gene: ZC84.6
A:Map position: 3
Query Match 22.7%; Score 347; DB 2; Length 1474;
Best Local Similarity 30.7%; Pred. No. 2.4e-20;
Matches 86; Conservative 33; Mismatches 95; Indels 66; Gaps 10;
Qy 22 MHSFCAFKADGPKCAIMKRFNIFTRQCEFIYGGCGNQRNFESLECKKMT----- 77
Db 435 MQTICTOPLRVGNCDSRVRYWYSAATRECSFEYTCQGNNDNNFETLVDCQTFCRNAP 494
Qy 78 -----RDNANRIKTLQOE-----KPDFCFLEEDPG- 104

Db 495 EPRCQGOAYKDNQKQKFTVTCTNROSSEPCANFECYFDGNMHGCCPTKATCTSLSPSPGK 554
QY 105 IC-RGYITRYFYNNOTKOCERFKYGGCLGNMNNFTLECKNICEDGPNQFQVDNYGTOL 163
Db 555 TCGPVGVSFKYHNPOTQCESFEYLGCDGNSWTFASRAECENYC--GVGG--CANGGSPL 610
QY 164 NAVNNSLTPQSTK---VPSLFEFFHGPSW-----CLTPADRG--LCRAN- 201
Db 611 RDSNGALQCSERDGGCFSSHECYGSLGPDWMSYRCCPTKTYICGLFPQQGSSSLCSGGL 670
QY 202 --ENRFYNSVIGKRPKRYSCGCGNENFTSKQECCLRAC 239
Db 671 TVVTRYFNIYTRKCSFPFYNGCDGNPNFNASLQCNFC 710

RESULT 12
T23573
hypothetical protein K103.4 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
R/McMurray, A.
submitted to the EMBL Data Library, June 1996
A/Reference number: Z19762
A/Accession: T23573
A/Status: preliminary; translated from GB/EMBL/DBDJ
A/Molecule type: DNA
A/Residues: 1-922 <WIL>
A/Cross-references: UNIPROT:Q21418; EMBL:Z75545; PIDN:CAA9886.1; GSPDB:GN00019; CESP:K103
A/Experimental source: clone K103
C/Genetics:
A/Gene: CESP:K103.4
A/Map position: 1
A/Introns: 60/1; 228/1; 278/1; 355/1; 743/1; 802/1; 885/2

Query Match 22.3%; Score 340; DB 2; Length 922;
Best Local Similarity 29.0%; Pred. No. 5.5e-20;
Matches 84; Conservative 45; Mismatches 93; Indels 68; Gaps 13;

QY 26 CAFRADDGPKAKIMKRRFFNIFTROCEFIYGGCGNORRPFESLECKKMC----- 76
Db 411 CKLPRQGNCTGYSNRWFWNAKTGNCCEFIYGGCGNANFTYKCEQDYCDARSFQC 470
QY 77 -----TRDNANRI-----KTLQOEKPDFCFLE-----EDPGI 105
Db 471 IQGTALTDGNGFIICGSSAATTCPAN--HYCVYDGTYYGCCPTQAYTCSLSVKSGAS 528
QY 106 CRGYITRYFYNNOTKOCERFKYGGCLGNMNNFTLECKNIC--EDGPNQFQV---DNYG 160
Db 529 CGPAVTRYDSTIRTCQTYSFNGCDGNSNMFATQQCKDYCRVESCPDGEVWKEQNGA 588
QY 161 TQLNAVNS-----LTQSTKVPISLFEFHG---PS---WCLTPADRG--CRANE-NRFY 206
Db 589 ARACITNRQCPSTHYCTPVTWTGTVYTKSLCPSKFNVCSPQDRVGVRCSTFISRWY 648
QY 207 YNSVIGKRPKRYSCGCGNENFTSKQEC-----LRACKGFIORISKGG 251
Db 649 FNADSKTQCTEYNGCEGNRNFNFSQSKQNYCLSEACPPTGV--VAKDG 696

RESULT 13
H88380
protein T22F7.3 [imported] - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
R/anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A/Reference number: A75000; MUID:99069613; PMID:9851916
A/Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.ele
A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A/Accession: H88380

A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1522 <STO>
A/Cross-references: GB:chr_III; PIDN:AAA20672.1; PID:g529714; GSPDB:GN00021; CESP:T22F7.
A/Note: highly similar to ZC84.1
C/Genetics:
A/Gene: T22F7.3
A/Map position: 3

Query Match 21.9%; Score 334.5; DB 2; Length 1522;
Best Local Similarity 28.2%; Pred. No. 2.7e-19;
Matches 90; Conservative 40; Mismatches 90; Indels 99; Gaps 14;

QY 24 SFCAFKADDGPKAKIMKRRFFNIFTROCEFIYGGCGNORRPFESLECKKMCCT----- 77
Db 531 SLCTQPKELGDCISAVRYWYNAATRCSEMFQYTGCGNDNNTLMACQCKRGHVEP 590
QY 78 -----RDNANRIKTLQOEKPD-----FCFLEEDPGI-C 106
Db 591 KQHGAFRDRNGNFQCSDKQNGPKCPVNVYCSFDGTTGCGCTKATCTSLNPKGVQC 650
QY 107 ---RGYITRYFYNNOTKOCERFKYGGCLGNMNNFTLECKNICEDG--PNGFQVDNYGT 161
Db 651 GSGRSY--RYFNSNKQSCSFQYEGCDGNANFLTSEDCHYCGVGCGPNG-----GM 702
QY 162 QL--NAVNSLTPQSTK-VPSLFEFFHGPSWCLT-----PADRGLC----- 198
Db 703 PLRDEATKPMSCSEQKSCPSSTHE-----CLTTPVNHVGSRCCTPKQHICSQPPQGN 756
QY 199 ---RANRFRYNSVIGKRPKRYSCGCGNENFTSKQECCLRACKGFIORISKGLIKT 255
Db 757 HCSKISVGRFYFNIIVTRECATTQYNGCGNGLNPNFATQSECNFCS-----SAGCAVG- 808
QY 256 KRREKKQKRVKAYEEIFVK 274
Db 809 -----EVAYKDVNTK 818

RESULT 14
E88550
protein ZC84.1 [imported] - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: E88550
R/anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A/Reference number: A75000; MUID:99069613; PMID:9851916
A/Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.ele
A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A/Accession: E88550
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1416 <STO>
A/Cross-references: UNIPROT:Q03610; GB:chr_III; PIDN:CAA9569.1; PID:g3881446; GSPDB:GN0
A/Note: similar to Serine protease inhibitor, Kunitz type
C/Genetics:
A/Gene: ZC84.1
A/Map position: 3

Query Match 21.8%; Score 332.5; DB 2; Length 1416;
Best Local Similarity 31.6%; Pred. No. 3.6e-19;
Matches 87; Conservative 29; Mismatches 92; Indels 67; Gaps 11;

QY 24 SFCAFKADDGPKAKIMKRRFFNIFTROCEFIYGGCGNORRPFESLECKKMCCTRDNANR 83
Db 432 TICAPLRIGDCTENKRYWYNAATRCQMFETTGCGNDNNTLSDCNFC--KNAIP 489
QY 84 IIKTLQOEKPDF-----CFLEEDPGI-C- 106
Db 490 EPKICIQQAYKDMFGNFTVCSNGMGCPANVECYFDGSGWCCPCTKATCTSLNDSGIQCG 549
QY 107 RGYITRYFYNNOTKOCERFKYGGCLGNMNNFTLECKNICEDG--PNGFQVDNYGTOLN 164

```
Db      550 AGSTFKYYNQTCNCESFQYNGCDGNSNNFANRDACESYCSVGGCPNG-----GTPLR 603
Qy      165 AVNNSLT---PQSTKVP-----SLFEFHGPS---WCLTPADRGL-CRAN-ENR 204
Db      604 DHSGMWVWCGAQQTSCPDSCHECIPVLVGNLSLNRCCPTRAYMCGLPPOQGTCCGANYVQR 663
Qy      205 FYNSVICKCRPFKYSGCGGNNFTSKOECLRAC 239
Db      664 YFNIIVTSQCTSFQFGGCDGNANFLNIQQRNFC 698
```

RESULT 15

S28291

hypochemical protein ZC84.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C:Accession: S28291

R:Thomas, K.

submitted to the EMBL Data Library, December 1992

A:Reference number: S28285

A:Accession: S28291

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-2844 <THO>

A:Cross-references: UNIPROT:Q03610; EMBL:Z19157

C:Genetics:

A:Introns: 14/1; 32/3; 57/1; 192/3; 277/1; 398/1; 439/1; 474/1; 497/1; 813/1; 1135/1; 12493/1; 2555/1; 2720/1; 2739/3; 2819/1
F:220-274/Domain: animal Kunitz-type proteinase inhibitor homology <BPI1>
F:343-395/Domain: animal Kunitz-type proteinase inhibitor homology <BPI2>
F:442-492/Domain: animal Kunitz-type proteinase inhibitor homology <BPI3>
F:546-598/Domain: animal Kunitz-type proteinase inhibitor homology <BPI4>
F:654-706/Domain: animal Kunitz-type proteinase inhibitor homology <BPI5>
F:1662-1716/Domain: animal Kunitz-type proteinase inhibitor homology <BPI6>
F:1787-1839/Domain: animal Kunitz-type proteinase inhibitor homology <BPI7>
F:1845-1895/Domain: animal Kunitz-type proteinase inhibitor homology <BPI8>
F:1952-2004/Domain: animal Kunitz-type proteinase inhibitor homology <BPI9>
F:2097-2152/Domain: animal Kunitz-type proteinase inhibitor homology <BPI10>

Query Match

21.8%; Score 332.5; DB 2; Length 2844;

Best Local Similarity 31.6%; Pred. No. 7.6e-19;

Matches 87; Conservative 29; Mismatches 92; Indels 67; Gaps 11;

Qy 24 SFCAFKADGPKCKALMKRFFNIFTRQCEEFYGGCEGNQNRFSLECKKXCTRDNANR 83

Db 440 TICAQPLRIGDCTENVKRYNARTQCMPFYTCQGNNDNFDSDIMDCQNF--KNAIP 497

Qy 84 IIKTTLQEKPDF-----CFLEEDPGI-C- 106

Db 498 EPKCIQQAQYKDMFGNFTVCSNGMGCPANYCYFDGQWGCPCPKAFTCSLNTDSGIQCG 557

Qy 107 RGYITRYFYNNQTKOCERFKYGGCLGNMNFETLEECNICEDG--PNGFQVDNYGTOLN 164

Db 558 AGSTFKYYNQTCNCESFQYNGCDGNSNNFANRDACESYCSVGGCPNG-----GTPLR 611

Qy 165 AVNNSLT---PQSTKVP-----SLFEFHGPS---WCLTPADRGL-CRAN-ENR 204

Db 612 DHSGMWVWCGAQQTSCPDSCHECIPVLVGNLSLNRCCPTRAYMCGLPPOQGTCCGANYVQR 671

Qy 205 FYNSVICKCRPFKYSGCGGNNFTSKOECLRAC 239

Db 672 YFNIIVTSQCTSFQFGGCDGNANFLNIQQRNFC 706

Search completed: April 16, 2005, 03:28:47

Job time : 46 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 16, 2005, 03:21:23 ; Search time 43 Seconds
(without alignments)
479.143 Million cell updates/sec

Title: US-10-753-079-1

Perfect score: 1528

Sequence: 1 DSEEDERTITDTLPLK.....RRKKQKVYKIAEYIFVQNM 276

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1528	100.0	276	2	US-08-796-850-1
2	1528	100.0	276	4	Sequence 1, Appli
3	1528	100.0	277	1	Sequence 1, Appli
4	1528	100.0	304	1	Sequence 2, Appli
5	1528	100.0	304	1	Sequence 9, Appli
6	1528	100.0	304	1	Sequence 18, Appli
7	1528	100.0	304	2	Sequence 18, Appli
8	1528	100.0	304	3	Sequence 1, Appli
9	1528	100.0	304	3	Sequence 25, Appli
10	1528	100.0	304	3	Sequence 1, Appli
11	1528	100.0	304	3	Sequence 1, Appli
12	1528	100.0	304	3	Sequence 25, Appli
13	1528	100.0	304	4	Sequence 1, Appli
14	1528	100.0	304	4	Sequence 16, Appli
15	1528	100.0	304	6	Patent No. 5466783
16	1528	100.0	304	6	Patent No. 5466783
17	1528	100.0	352	3	Sequence 2, Appli
18	1528	100.0	352	5	Sequence 2, Appli
19	1528	100.0	381	4	Sequence 7400, Ap
20	1525	99.8	276	1	Sequence 9, Appli
21	1525	99.8	276	1	Sequence 9, Appli
22	1525	99.8	276	1	Sequence 9, Appli
23	1525	99.8	276	3	Sequence 9, Appli
24	1525	99.8	276	3	Sequence 9, Appli
25	1525	99.8	276	4	Sequence 9, Appli
26	1525	99.8	276	5	Sequence 9, Appli
27	1525	99.8	276	5	Sequence 9, Appli

28 1522 99.6 304 3 US-09-054-782-2 Sequence 2, Appli
29 1522 99.6 304 4 US-09-627-676-2 Sequence 2, Appli
30 1522 99.6 304 4 US-10-377-817-2 Sequence 2, Appli
31 1521 99.5 276 1 US-07-828-920A-1 Sequence 1, Appli
32 1517 99.3 304 4 US-09-763-565-2 Sequence 2, Appli
33 1507 98.6 304 4 US-09-763-565-4 Sequence 4, Appli
34 1447.5 94.7 291 4 US-10-000-489-48 Sequence 48, Appli
35 1444.5 94.5 291 4 US-10-000-489-52 Sequence 52, Appli
36 1180.5 77.3 213 6 5466783-25 Patent No. 5466783
37 1180.5 77.3 213 6 5466783-25 Patent No. 5466783
38 900 58.9 189 1 US-07-828-920A-7 Sequence 7, Appli
39 897 58.7 161 1 US-08-437-841-19 Sequence 19, Appli
40 897 58.7 161 1 US-08-286-521-19 Sequence 19, Appli
41 897 58.7 161 1 US-08-436-175-19 Sequence 19, Appli
42 897 58.7 161 3 US-08-943-682-19 Sequence 19, Appli
43 897 58.7 161 4 US-09-741-106-19 Sequence 19, Appli
44 897 58.7 161 5 PCT-US95-09464-19 Sequence 19, Appli
45 834 54.6 183 1 US-07-828-920A-5 Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-796-850-1
; Sequence 1, Application US/08796850
; Patent No. 5981471
; GENERAL INFORMATION:
; APPLICANT: Papathanassiou, Adonia E
; APPLICANT: Green, Shawn J.
; TITLE OF INVENTION: Compositions and Methods for Inhibiting
; TITLE OF INVENTION: Cellular Proliferation
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: U.S.A.
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/796,850
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Greene, Jamie L.
; REGISTRATION NUMBER: 32,467
; REFERENCE/DOCKET NUMBER: 05213-0290
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 818-3700
; TELEFAX: (404) 818-3799
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 276 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Active-site
; LOCATION: 2..3
; OTHER INFORMATION: /note= "Site of partial phosphorylation"

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FEATURE:
NAME/KEY: Active-site
LOCATION: 117..118
OTHER INFORMATION: /note= "Potential site for N-linked
OTHER INFORMATION: glycosylation"
FEATURE:
NAME/KEY: Active-site
LOCATION: 167..168
OTHER INFORMATION: /note= "Potential site for N-linked
OTHER INFORMATION: glycosylation"
FEATURE:
NAME/KEY: Active-site
LOCATION: 228..229
OTHER INFORMATION: /note= "Potential site for N-linked
OTHER INFORMATION: glycosylation"
FEATURE:
NAME/KEY: Domain
LOCATION: 26..76
OTHER INFORMATION: /label= Kunitz-1
FEATURE:
NAME/KEY: Domain
LOCATION: 97..147
OTHER INFORMATION: /label= Kunitz-2
FEATURE:
NAME/KEY: Domain
LOCATION: 189..239
OTHER INFORMATION: /label= Kunitz-3
US-08-796-850-1

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Query Match 100.0%; Score 1528; DB 2; Length 276;
Best Local Similarity 100.0%; Pred. No. 1.1e-145;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEEHTIITDLPPLKMHSCAFKADGPKAKMKRFFNFTRQCEEFYGGCE 60
DB 1 DSEDEEHTIITDLPPLKMHSCAFKADGPKAKMKRFFNFTRQCEEFYGGCE 60
QY 61 GNQRFESLECKKQCTRDNANRIKTTLOQEKDPDFCFLEEDPGICRGYITRYFYNNOTK 120
DB 61 GNQRFESLECKKQCTRDNANRIKTTLOQEKDPDFCFLEEDPGICRGYITRYFYNNOTK 120
QY 121 QCEKYGGCLGNMNFETLECKNICEDGPNQFQVNDYGTOLNANNLSLTPQSTKVPSL 180
DB 121 QCEKYGGCLGNMNFETLECKNICEDGPNQFQVNDYGTOLNANNLSLTPQSTKVPSL 180
QY 181 FEFHGPSWCLTPADRGLCRANENRYNSVIGKCRPFYSGCGNENFTSKQECCLACK 240
DB 181 FEFHGPSWCLTPADRGLCRANENRYNSVIGKCRPFYSGCGNENFTSKQECCLACK 240
QY 241 KGFIQIRISKGLIKTKRKRRKQKVIAEIEIFVKNM 276
DB 241 KGFIQIRISKGLIKTKRKRRKQKVIAEIEIFVKNM 276

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RESULT 2
US-09-766-778-1
Sequence 1, Application US/09766778
Patent No. 6734163
GENERAL INFORMATION:
APPLICANT: Papathanassiou, Adonia E
Green, Shawn J.
TITLE OF INVENTION: Compositions and Methods for Inhibiting
Cellular Proliferation
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.A.
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,778
FILING DATE: 22-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/227,955
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Greene, Jamie L.
REGISTRATION NUMBER: 32,467
REFERENCE/DOCKET NUMBER: 05213-0290
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 818-3700
TELEFAX: (404) 818-3799
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: Active-site
LOCATION: 2..3
OTHER INFORMATION: /note= "Site of partial
phosphorylation"
FEATURE:
NAME/KEY: Active-site
LOCATION: 117..118
OTHER INFORMATION: /note= "Potential site for N-linked
glycosylation"
FEATURE:
NAME/KEY: Active-site
LOCATION: 167..168
OTHER INFORMATION: /note= "Potential site for N-linked
glycosylation"
FEATURE:
NAME/KEY: Active-site
LOCATION: 228..229
OTHER INFORMATION: /note= "Potential site for N-linked
glycosylation"
FEATURE:
NAME/KEY: Domain
LOCATION: 26..76
OTHER INFORMATION: /label= Kunitz-1
FEATURE:
NAME/KEY: Domain
LOCATION: 97..147
OTHER INFORMATION: /label= Kunitz-2
FEATURE:
NAME/KEY: Domain
LOCATION: 189..239
OTHER INFORMATION: /label= Kunitz-3
US-09-766-778-1
SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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Query Match 100.0%; Score 1528; DB 4; Length 276;
Best Local Similarity 100.0%; Pred. No. 1.1e-145;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEEHTIITDLPPLKMHSCAFKADGPKAKMKRFFNFTRQCEEFYGGCE 60
DB 1 DSEDEEHTIITDLPPLKMHSCAFKADGPKAKMKRFFNFTRQCEEFYGGCE 60
QY 61 GNQRFESLECKKQCTRDNANRIKTTLOQEKDPDFCFLEEDPGICRGYITRYFYNNOTK 120

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Db 61 GQNRFSLECKKQCTDNNR11KTLQEKDPFCFLEEDPGICRGYITRYFNNQTK 120
Qy 121 QCFKYGGCLGNMNFETLECKNICEDGPNQFVDNYGTQLNANVNSLTPOSTKVPSSL 180
Db 121 QCFKYGGCLGNMNFETLECKNICEDGPNQFVDNYGTQLNANVNSLTPOSTKVPSSL 180
Qy 181 FEFHGPSWCLTPADRGCLCRANENRFFYNVSGKCRPFKYSGCGNENFTSKQECRLACK 240
Db 181 FEFHGPSWCLTPADRGCLCRANENRFFYNVSGKCRPFKYSGCGNENFTSKQECRLACK 240
Qy 241 KGFIORISKGLIKTKRKRKQKQVIAEYEEIFVKNM 276
Db 241 KGFIORISKGLIKTKRKRKQKQVIAEYEEIFVKNM 276

RESULT 3
US-07-844-297-1
; Sequence 1, Application US/07844297
; Patent No. 5212091
; GENERAL INFORMATION:
; APPLICANT: Diaz-Collier, Judy A.
; APPLICANT: Gustafson, Mark E.
; APPLICANT: Wun, Tze-Chien
; TITLE OF INVENTION: Method of Producing Tissue Factor
; TITLE OF INVENTION: Pathway Inhibitor
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 63167

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/844,297
; FILING DATE: 19920302
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: 07-21(819)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-844-297-1

Query Match 100.0%; Score 1528; DB 1; Length 277;
Best Local Similarity 100.0%; Pred. No. 1.1e-145;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DSEDEEHTITDTELPPLKLMHSFCAPKADGPKCAIMKRPFFNIFTRQCEEFYGGCE 60
Db 2 DSEDEEHTITDTELPPLKLMHSFCAPKADGPKCAIMKRPFFNIFTRQCEEFYGGCE 61
Qy 61 GQNRFSLECKKQCTDNNR11KTLQEKDPFCFLEEDPGICRGYITRYFNNQTK 120
Db 62 GQNRFSLECKKQCTDNNR11KTLQEKDPFCFLEEDPGICRGYITRYFNNQTK 121
Qy 121 QCFKYGGCLGNMNFETLECKNICEDGPNQFVDNYGTQLNANVNSLTPOSTKVPSSL 180
Db 122 QCFKYGGCLGNMNFETLECKNICEDGPNQFVDNYGTQLNANVNSLTPOSTKVPSSL 181

Qy 181 FEFHGPSWCLTPADRGCLCRANENRFFYNVSGKCRPFKYSGCGNENFTSKQECRLACK 240
Db 182 FEFHGPSWCLTPADRGCLCRANENRFFYNVSGKCRPFKYSGCGNENFTSKQECRLACK 241
Qy 241 KGFIORISKGLIKTKRKRKQKQVIAEYEEIFVKNM 276
Db 242 KGFIORISKGLIKTKRKRKQKQVIAEYEEIFVKNM 277

RESULT 4
US-08-026-145-2
; Sequence 2, Application US/08026145
; Patent No. 5378614
; GENERAL INFORMATION:
; APPLICANT: Petersen, Jens G. Liteke
; APPLICANT: No. 5378614dfang, Ole Juul
; TITLE OF INVENTION: Method for Making TFPI Analogues
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5378614 No. 5378614disk of No. 5378614th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6200
; CITY: New York
; STATE: N. Y.
; COUNTRY: United States of America
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/026,145
; FILING DATE: 19930302
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/828,920
; FILING DATE: 27-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DK/90/00212
; FILING DATE: 17-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 4080/89
; FILING DATE: 18-AUG-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Agtis, Cheryl H.
; REGISTRATION NUMBER: 34086
; REFERENCE/DOCKET NUMBER: 3321.214-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 304 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-026-145-2

Query Match 100.0%; Score 1528; DB 1; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.2e-145;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DSEDEEHTITDTELPPLKLMHSFCAPKADGPKCAIMKRPFFNIFTRQCEEFYGGCE 60
Db 29 DSEDEEHTITDTELPPLKLMHSFCAPKADGPKCAIMKRPFFNIFTRQCEEFYGGCE 88
Qy 61 GQNRFSLECKKQCTDNNR11KTLQEKDPFCFLEEDPGICRGYITRYFNNQTK 120
Db 89 GQNRFSLECKKQCTDNNR11KTLQEKDPFCFLEEDPGICRGYITRYFNNQTK 148
Qy 121 QCFKYGGCLGNMNFETLECKNICEDGPNQFVDNYGTQLNANVNSLTPOSTKVPSSL 180
Db 149 QCFKYGGCLGNMNFETLECKNICEDGPNQFVDNYGTQLNANVNSLTPOSTKVPSSL 208

Qy	181	FEFHGSWCLTTPADRLCRANENRFFYNSVTGKCPFFKSCGCGNENFTSKQECIRACK	240
Db	209	FEFHGSWCLTTPADRLCRANENRFFYNSVTGKCPFFKSCGCGNENFTSKQECIRACK	268
Qy	241	KGFIQIRISKGLLTKTKRKKQKRVIAYEIEFVKQM	276
Db	269	KGFIQIRISKGLLTKTKRKKQKRVIAYEIEFVKQM	304

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RESULT 5
US-08-446-646--9
; Sequence 9, Application US/08446646
; Patent No. 5726038
; GENERAL INFORMATION:
; APPLICANT: Christiansen, Lars
; APPLICANT: Petersen, Jens G.
; TITLE OF INVENTION: A DNA Construct Encoding the YAP3 Signal
; TITLE OF INVENTION: Peptide
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5726038o No. 5726038disk of No. 5726038th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,646
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3987.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 304 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-646-9

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Query Match	100.0%;	Score 1528;	DB 1;	Length 304;
Best Local Similarity	100.0%;	Pred. No. 1.2e-145;		
Matches 276;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	DSBEDEHTIIITTELPPLKMHSPCAFKADGGCKAIMKRFNFNITRQCEEEFYGGCE	60	
Db				
QY	29	DSBEDEHTIIITTELPPLKMHSPCAFKADGGCKAIMKRFNFNITRQCEEEFYGGCE	88	
Db				
QY	61	GNQNRFESELECKKMCITRDNANRIIKTTLQOEKPDFCFLEEDPGICRGYITRIFYNNQTK	120	
Db				
QY	89	GNQNRFESELECKKMCITRDNANRIIKTTLQOEKPDFCFLEEDPGICRGYITRIFYNNQTK	148	
Db				
QY	121	QCERFKYGGCLGNMNPFTTLEECKNICEDGPGFQVDNYGTQLNAVNSLTPQSTKVPSL	180	
Db				
QY	149	QCERFKYGGCLGNMNPFTTLEECKNICEDGPGFQVDNYGTQLNAVNSLTPQSTKVPSL	208	
Db				
QY	181	FEFHGFSWCLTTPADRGLCRANERNFYNSVIGKCRPEKYGCGGNNENNFTSKQECIRACK	240	
Db				
QY	209	FEFHGFSWCLTTPADRGLCRANERNFYNSVIGKCRPPFKYGCGGNNENNFTSKQECIRACK	268	
Db				
QY	241	KGFIQRISKGLIKTKRKRKKQRVKIAYEEIFVKNM	276	
Db				

Db 269 KGFIQRISGGLIKTKRKRKKQVRVKIAYEEIFVKNM 304

RESULT 6

US-08-676-125A-18
 ; Sequence 18, Application US/08676125A
 ; Patent No. 5795865
 ; GENERAL INFORMATION:
 ; APPLICANT: MARKLAND, William
 ; APPLICANT: LADNER, Robert Charles
 ; TITLE OF INVENTION: KALLIKREIN-INHIBITING "KUNITZ DOMAIN" PROTEINS AND ANALOGUES
 ; NUMBER OF SEQUENCES: 70
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Yankwich & Associates
 ; STREET: 130 Bishop Allen Drive, fifth floor
 ; CITY: Cambridge
 ; STATE: Massachusetts
 ; COUNTRY: United States of America
 ; ZIP: 02139
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Word for Windows 6.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/676,125A
 ; FILING DATE: 25 September 1996
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION NUMBER:
 ; APPLICATION NUMBER: PCT/US95/00299
 ; FILING DATE: 11 January 1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/179,964
 ; FILING DATE: 11 January 1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/208,264
 ; FILING DATE: 10 March 1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: YANKWICH, Leon R.
 ; REGISTRATION NUMBER: 30,237
 ; REFERENCE/DOCKET NUMBER: DYX-006.2P US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 491-4343
 ; TELEFAX: (617) 491-8801
 ; INFORMATION FOR SEQ ID NO: 18:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 304 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-676-125A-18

Query Match 100.0%; Score 1528; DB 1; Length 304;
 Best Local Similarity 100.0%; Pred. No. 1.2e-145;
 Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEHTIITDTELPPLKLMHSFCAFKADDDGCKAIKKEFFNFIFTRQCEEFYVGCE 60
 Db 29 DSEDEHTIITDTELPPLKLMHSFCAFKADDDGCKAIKKEFFNFIFTRQCEEFYVGCE 88
 QY 61 GNQRRFESLECKKMCITRDNANRIKTTLOQKPDPCFLEEDPGICRGYITRYFYNNQTK 120
 Db 89 GNQRRFESLECKKMCITRDNANRIKTTLOQKPDPCFLEEDPGICRGYITRYFYNNQTK 148
 QY 121 QCRFRYGGCLGNWNNFETILEECKNICEDGPNGFQVDNYGTQLNAVNNSLTPQSTKVPSL 180
 Db 149 QCRFRYGGCLGNWNNFETILEECKNICEDGPNGFQVDNYGTQLNAVNNSLTPQSTKVPSL 208
 QY 181 FEPHGSWCLTPADRGLCRANENRFFYNSVIGKRPFKYSCGGNENNFTSKQECIRACK 240
 Db 209 FEPHGSWCLTPADRGLCRANENRFFYNSVIGKRPFKYSCGGNENNFTSKQECIRACK 268

Qy 241 KGFIORISKGLIKTKRKRKORVKIAYEIEFVKNM 276
Db 269 KGFIORISKGLIKTKRKRKORVKIAYEIEFVKNM 304

RESULT 7

US-09-136-012A-18
; Sequence 18, Application US/09136012A
; Patent No. 5994125
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP
; APPLICANT: MARKLAND, William
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: KALLIKREIN-INHIBITING "KUNITZ DOMAIN" PROTEINS
; TITLE OF INVENTION: AND ANALOGUES THEREOF
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive, fifth floor
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5-inch diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: Microsoft Word 97 SR-1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136.012A
; FILING DATE: 17-August-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/676,125
; FILING DATE: 25-September-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00299
; FILING DATE: 11-January-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/208,264
; FILING DATE: 10-March-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/179,964
; FILING DATE: 11-January-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: YANKWICH, Leon R.
; REGISTRATION NUMBER: 30,237
; NAME: ZWICKER, Kenneth P.
; REGISTRATION NUMBER: 43,310
; REFERENCE/DOCKET NUMBER: DYX-006.2P US-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 491-4343
; TELEFAX: (617) 491-8801
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 304 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-136-012A-18

Query Match 100.0%; Score 1528; DB 2; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.2e-145;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DSEDEEHTITDTELPPLKLMHSFCAPKADGPKAIMKFFNIFTRQCEEFYGGCE 60
Db 29 DSEDEEHTITDTELPPLKLMHSFCAPKADGPKAIMKFFNIFTRQCEEFYGGCE 88
Qy 61 GQNRFSLEBCKKMCCTRDNANRIKTTLOQEKPDFCFLEEDPGICRGYITRYFNNQTK 120
Db 89 GQNRFSLEBCKKMCCTRDNANRIKTTLOQEKPDFCFLEEDPGICRGYITRYFNNQTK 148

Qy 121 QCERFKYGGCLGNMNFETLEECKNICEDGNGFQVDNYGTOLNANNSLTPQSTKVPSL 180
Db 149 QCERFKYGGCLGNMNFETLEECKNICEDGNGFQVDNYGTOLNANNSLTPQSTKVPSL 208
Qy 181 FEFHGPSWCLTPADRGLCRANENRFYNSVIGKCRPFKYSGCGGNENFTSKQECLRACK 240
Db 209 FEFHGPSWCLTPADRGLCRANENRFYNSVIGKCRPFKYSGCGGNENFTSKQECLRACK 268
Qy 241 KGFIORISKGLIKTKRKRKORVKIAYEIEFVKNM 276
Db 269 KGFIORISKGLIKTKRKRKORVKIAYEIEFVKNM 304

RESULT 8

US-08-676-124-1
; Sequence 1, Application US/08676124
; Patent No. 6010880
; GENERAL INFORMATION:
; APPLICANT: MARKLAND, William
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: INHIBITORS OF HUMAN PLASMIN DERIVED
; TITLE OF INVENTION: FROM FROM THE KUNITZ DOMAINS
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/676,124
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00298
; FILING DATE: 11-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/179,658
; FILING DATE: 11-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/208,265
; FILING DATE: 10-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, IVER P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: MARKLAND=3B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 304 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-676-124-1

Query Match 100.0%; Score 1528; DB 3; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.2e-145;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DSEDEEHTITDTELPPLKLMHSFCAPKADGPKAIMKFFNIFTRQCEEFYGGCE 60
Db 29 DSEDEEHTITDTELPPLKLMHSFCAPKADGPKAIMKFFNIFTRQCEEFYGGCE 88
Qy 61 GQNRFSLEBCKKMCCTRDNANRIKTTLOQEKPDFCFLEEDPGICRGYITRYFNNQTK 120

Db 89 GQNRFSLECKKCMCTRDNANRIKTTIQEKPDPFCFLEEDPGICRGYITRYFNNQTK 148
QY 121 QCFRFGYGGCLGNMNNFETLECKNICEDGPNQFQVNDYGTOLNANNVNSLTPOSTKVPSEL 180
Db 149 QCFRFGYGGCLGNMNNFETLECKNICEDGPNQFQVNDYGTOLNANNVNSLTPOSTKVPSEL 208
QY 181 FEFHGPSWCLTPADRGCLCRANENRFFYNSVIGKCRPFKYSGCGGNNFTSKQECCLACK 240
Db 209 FEFHGPSWCLTPADRGCLCRANENRFFYNSVIGKCRPFKYSGCGGNNFTSKQECCLACK 268
QY 241 KGFIQRIKSGGLIKTKRKRKQKQVIAVEEIFFVKNM 276
Db 269 KGFIQRIKSGGLIKTKRKRKQKQVIAVEEIFFVKNM 304

RESULT 9

US-08-208-264A-25
; Sequence 25, Application US/08208264A
; Patent No. 6057287

; GENERAL INFORMATION:
; APPLICANT: MARKLAND, William
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: KALLIKREIN-BINDING "KUNITZ DOMAIN"
; TITLE OF INVENTION: PROTEINS AND ANALOGUES THEREOF
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5-inch diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 95
; SOFTWARE: Microsoft Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/208,264A
; FILING DATE: 10-MAR-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/179,964
; FILING DATE: 11-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Leon R. Yankwich
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: DYX-006.1 US
; TELEPHONE: 617-491-4343
; TELEFAX: 617-491-8801
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 304 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-208-264A-25

Query Match 100.0%; Score 1528; DB 3; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.2e-145;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEEHITDTLPLKLMHSPKADDPCKALMKRFFNIFTRQCEEFYGGCE 60
Db 29 DSEDEEHITDTLPLKLMHSPKADDPCKALMKRFFNIFTRQCEEFYGGCE 88
QY 61 GQNRFSLECKKCMCTRDNANRIKTTIQEKPDPFCFLEEDPGICRGYITRYFNNQTK 120
Db 89 GQNRFSLECKKCMCTRDNANRIKTTIQEKPDPFCFLEEDPGICRGYITRYFNNQTK 148

QY 121 QCFRFGYGGCLGNMNNFETLECKNICEDGPNQFQVNDYGTOLNANNVNSLTPOSTKVPSEL 180
Db 149 QCFRFGYGGCLGNMNNFETLECKNICEDGPNQFQVNDYGTOLNANNVNSLTPOSTKVPSEL 208
QY 181 FEFHGPSWCLTPADRGCLCRANENRFFYNSVIGKCRPFKYSGCGGNNFTSKQECCLACK 240
Db 209 FEFHGPSWCLTPADRGCLCRANENRFFYNSVIGKCRPFKYSGCGGNNFTSKQECCLACK 268
QY 241 KGFIQRIKSGGLIKTKRKRKQKQVIAVEEIFFVKNM 276
Db 269 KGFIQRIKSGGLIKTKRKRKQKQVIAVEEIFFVKNM 304

RESULT 10

US-09-414-878-1
; Sequence 1, Application US/09414878
; Patent No. 6071723

; GENERAL INFORMATION:
; APPLICANT: DYAX CORP
; APPLICANT: MARKLAND, William
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: Inhibitors of Human Plamin Derived
; TITLE OF INVENTION: From The Kunitz Domains
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5-inch diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: Microsoft Word 97 SR-1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/414,878
; FILING DATE: (currently herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/240,136
; FILING DATE: 29-JAN-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/676,124
; FILING DATE: 07-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00298
; FILING DATE: 11-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/208,265
; FILING DATE: 10-MAR-1994
; APPLICATION NUMBER: 08/179,685
; FILING DATE: 11-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: YANKWICH, Leon R
; REGISTRATION NUMBER: 30,237
; NAME: ZWICKER, Kenneth P
; REGISTRATION NUMBER: 43,310
; REFERENCE/DOCKET NUMBER: DYX-007.2P US-2

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-491-4343
; TELEFAX: 617-491-8801
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 304 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-414-878-1

Query Match 100.0%; Score 1528; DB 3; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.2e-145; Indels 0; Gaps 0;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DSEDEEHTIITDTPPLKLMHSCAFKADGPKCKAIIKMFNFTSQCEEFYGGCE 60
DB 29 DSEDEEHTIITDTPPLKLMHSCAFKADGPKCKAIIKMFNFTSQCEEFYGGCE 88
QY 61 GQNRFSLEBCKKCTRDNANRII KTTLOQEKDPFCLEEDPGICRGYITRYFYNNQTK 120
DB 89 GQNRFSLEBCKKCTRDNANRII KTTLOQEKDPFCLEEDPGICRGYITRYFYNNQTK 148
QY 121 QCRFKYGGCLGNMNFETLECKNICEDGPNGFQVDNYGTOLNANNVNSLTPQSTKVPSL 180
DB 149 QCRFKYGGCLGNMNFETLECKNICEDGPNGFQVDNYGTOLNANNVNSLTPQSTKVPSL 208
QY 181 FEFHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFKYSGCGGNENFTSQCECLACK 240
DB 209 FEFHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFKYSGCGGNENFTSQCECLACK 268
QY 241 KGFQIRISKGLIKTKRKRKQVIAEIEIFVKM 276
DB 269 KGFQIRISKGLIKTKRKRKQVIAEIEIFVKM 304

RESULT 11

US-09-240-136-1
; Sequence 1, Application US/09240136
; Patent No. 6103499
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP
; APPLICANT: MARKLAND, William
; APPLICANT: LADNER, Robert C
; TITLE OF INVENTION: Inhibitors of Human Plamin Derived
; TITLE OF INVENTION: From The Kunitz Domains
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5-inch diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: Microsoft Word 97 SR-1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/240,136
; FILING DATE: (concurrently herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/676,124
; FILING DATE: 07-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00298
; FILING DATE: 11-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/208,265
; FILING DATE: 10-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/179,685
; FILING DATE: 11-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: YANKWICH, Leon R
; REGISTRATION NUMBER: 30,237
; NAME: ZWICKER, Kenneth P
; REGISTRATION NUMBER: 43,310
; REFERENCE/DOCKET NUMBER: DYX-007.2P US-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-491-4343
; TELEFAX: 617-491-8801

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 304 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-240-136-1

Query Match 100.0%; Score 1528; DB 3; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.2e-145;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DSEDEEHTIITDTPPLKLMHSCAFKADGPKCKAIIKMFNFTSQCEEFYGGCE 60
DB 29 DSEDEEHTIITDTPPLKLMHSCAFKADGPKCKAIIKMFNFTSQCEEFYGGCE 88
QY 61 GQNRFSLEBCKKCTRDNANRII KTTLOQEKDPFCLEEDPGICRGYITRYFYNNQTK 120
DB 89 GQNRFSLEBCKKCTRDNANRII KTTLOQEKDPFCLEEDPGICRGYITRYFYNNQTK 148
QY 121 QCRFKYGGCLGNMNFETLECKNICEDGPNGFQVDNYGTOLNANNVNSLTPQSTKVPSL 180
DB 149 QCRFKYGGCLGNMNFETLECKNICEDGPNGFQVDNYGTOLNANNVNSLTPQSTKVPSL 208
QY 181 FEFHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFKYSGCGGNENFTSQCECLACK 240
DB 209 FEFHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFKYSGCGGNENFTSQCECLACK 268
QY 241 KGFQIRISKGLIKTKRKRKQVIAEIEIFVKM 276
DB 269 KGFQIRISKGLIKTKRKRKQVIAEIEIFVKM 304

RESULT 12

US-09-421-097-25
; Sequence 25, Application US/09421097
; Patent No. 633402
; GENERAL INFORMATION:
; APPLICANT: MARKLAND, William
; APPLICANT: LADNER, Robert C
; TITLE OF INVENTION: KALLIKREIN-BINDING "KUNITZ DOMAIN"
; TITLE OF INVENTION: PROTEINS AND ANALOGUES THEREOF
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5-inch diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: Microsoft Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/421,097
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/208,264
; FILING DATE: 10-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/179,964
; FILING DATE: 11-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Leon R. Yankwich
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: DYX-006.1 US-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-491-4343
; TELEFAX: 617-491-8801

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